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Title:
Perfect score:
Sequence:
                                  Database :
                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       Minimum DB seq length: 0
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Gapop 10.0 , Gapext 0.5
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UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Q8zr03 salmonella		Q93nw6 streptomyce	Q7ny13 chromobacte	051674 borrelia bu	Q660el borrelia ga	Q9zlx3 helicobacte			Q9lip6 arabidopsis		-	Q810p2 helicobacte

ALIGNMENTS

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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [3] SEQUENCE OF 1-384 FROM N.A. Aumais J.P., Yu-Lee LY.; "Human 50 kD dynactin subunit, p50 dynamitin, isolated from HeLa cells."; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE OF 1-13.	SEQUENCE FROM N.A. TISSUE=Placenta, Skin, and Uterus; MEDLINE=2388857; pubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Liatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";	Dynactin complex 50 kDa shounit (50 kDa dynein-associated polypeptide) (p50 dynamitin) (DCTN-50) (Dynactin 2). Name=DCTN2; Synonyms=DCTN50; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1]	HUMAN STANDARD; PRT; 400 AA. DCT2 HUMAN STANDARD; PRT; 400 AA. Q13561; Q86YN2; Q9BW17; 01-NOV-1997 (Rel. 35, Created) 05-JUL-2004 (Rel. 44, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) DCT-2004 (Rel. 44, Last annotation update)

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RESULT DCT2_MC ID DCT2_MC QS AC QS DT 055 DT
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Best Local :
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28-FEB-2003 (Rel. 41, Createu)
05-JUL-2004 (Rel. 44, Last sequence of the complex of the complex of the submitted of the complex of t
                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
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EMBL; BC009468; AAH09468.1; --
EMBL; BC014083; AAH14083.1; --
EMBL; AY189155; AAO34395.1; --
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                                                                                                                                                                                                                                                         Dynactin complex 50 kDa su (p50 dynamitin) (DCTN-50) 23-48K) (GMP23-48K).
                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                          Name=Dctn2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99KJ8;
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gevaert K., Goethals M., Martens L., Thomas G.R., Vandekerckhove J.;
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GO:0005869; C:dynactin complex; TAS.
GO:0000776; C:kinetochore; TAS.
GO:0008283; P:cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Modulates cytoplasmic dynein binding to an organelle, and plays a role in prometaphase chromosome alignment and spind organization during mitosis. May play a role in synapse formati during brain development.

SUBUNIT: Subunit of dynactin, a multiprotein complex associated in the state of the synapse of the subunit of dynactin, a multiprotein complex associated in the synapse of the s
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erPro; IPR006996; Dynamitin.
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als M., Martens L., Van Damme J., Sta
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A -> AFAQEL (in Ref. 1).
E -> ELE (in Ref. 3).
LATV -> POHS (in Ref. 3).
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RA Strausberg R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Barcha A., Rodrigues S., Sanchez A.,
RA Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.A.;
RA Schuernich A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.";
RT Proc. Marl Acad Scii II s A Galfaga 1600170001
Query Match
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Matches 29
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                                                                                       Membrane, Microtubule; Motor protein.
INIT MET 0 By Sinilarity.
DOMAIN 98 131 Coiled coil (Potential).
DOMAIN 214 244 Coiled coil (Potential).
SEQUENCE 401 AA; 43985 MW; 1535E4ABD5940EBC CRC64;
                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
TISSUE=Brain;
MEDLINE=97289622; PubMed=9144527; DOI=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 65-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=22388257;
                                                                                                                                                                                                                   Coiled coil; Cytoskeleton; Direct protein sequencing;
                                                                                                                                                                                                                                         Pfam; PF04912; Dynamitin; 1.
                                                                                                                                                                                                                                                                                      MGD; MGI:107733;
                                                                                                                                                                                                                                                                                                               EMBL; BC004613; AAH04613.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21376052; PubMed=11483508; DOI=10.1093/emboj/20.15.4041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH BICD2
                                                                                                                                                                                                                                                                  InterPro; IPR006996; Dynamitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O J. 20:4041-4054(2001).

FUNCTION: Modulates Cytoplasmic dynein binding to an organelle, FUNCTION: Modulates Cytoplasmic dynein binding to an organelle, and plays a role in prometaphase chromosome alignment and spindle organization during mitosis. May play a role in synapse formation during brain development.

SUBCHIT: Subunit of dynactin, a multiprotein complex associated with dynein (By similarity). Interacts with BICD2.

SUBCELIULAR LOCATION: Cytoplasmic and membrane-associated.

DEVELOPMENTAL STAGE: Present thigh levels in both cytoplasmic between the played the membrane-associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated form are greatly reduced in the adult.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane-associated forms in neonates. Levels of membrane-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biophys. Res. Commun. 233:295-299(1997).
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401
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the 50-kDa subunit of
                                                                                                                                                                                                                                                                                           Dctn2.
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96.7%;
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AND DEVELOPMENTAL STAGE.
                        Score 135; DB 1;
Pred. No. 4.5e-09;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casminci P., Prange C.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodersren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Holkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Kzzywinski M.I., Skalska U., Smailus D.B., Scherch A., Schein J.E.,
W. Green S.J., Marra M.A.,
W. Green S.J., Marra M.A.,
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Best Local 9
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Q6AYH5;
25-OCT-2004
                                                                                 Q7ZXY2; PRELIMINARY; PRT;
Q7ZXY2; PRELIMINARY; PRT;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last seq
Q1-QCT-2003 (TrEMBLrel. 25, Last ann
Dctn2-prov protein.
Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Crania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC079042; AAH79042.1; -.
GO; GO:0005869; C:dynactin complex; IEA.
GO; GO:0007017; P:microtubule-based process; IEA.
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PubMed=12477932; DOI=10.1073/pnas.242603899;
PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Stenmen C.M., St
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Name=Dctn2;
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Director MGC Project;
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25-OCT-2004
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c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 4.5e-09;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Da J. Marra M. A., Schalks D.E., Schnerch A., Schein J.E.,
Da J. Marra M. A., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Da J. Marra M. A., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Da J. Marra M. A., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,
Da J. Marra M. A., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,
Da J. Marra M. A., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Name=dctn2-prov;
Xenopus laevis (African clawed frog).
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC044069; AAH44069.1; -.
GO; GO:0005869; C:dynactin complex; IEA.
GO; GO:0007017; P:microtubule-based process; IEA.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                             NCBI_TaxID=8355;
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"Generation and initial analysis of more than 15,000 full-length human
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Xenopodinae; Xenopus.
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c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Pred. No. 2e-06;
4; Mismatches
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AS trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
AS Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
AN Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Wagner P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Robert S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
A Richards S., Worley C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Richards S., Worley A.C., Shevchenko Y., Bouffard G.G.,
A Wilting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local (
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; EC070987; AAH70987.1; -.
GO; GO:0005869; C:dynactin complex; IEA.
GO; GO:0007017; P:microtubule-based process; IEA.
                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                     MGC82128 protein.
Name=MGC82128;
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25-OCT-2004
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                               TISSUE=Kidney;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton
Richardson P.;
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                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                             _TaxID=8355;
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                                                                                                                                                    FROM N.A.
   and genomic tools
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for Xenopus research: The NIH Xenopus
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Last annotation updat
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Pred. No. 2.3e-06;
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RX Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RX Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RX Hopkins R.F., Jordan H., Moore T., Max R., Robards T.E., Prange C.,
RX Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RX Richards S., Worley K.C., Hale S., Garcia A.M., Schibs R.A.,
RX Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RX Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RX Hilalon D.K., Walsha A., Young A.C., Shevchenko Y., Bouffard G.G.,
RX Habey J., Helton B., Ketteman M., Green E.D., Dickson M.C.,
RX Habey J., Walsha A., Touch R.J., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RX Arryen RA, M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RX Arryen RS, J. Marryen M.A.
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MEDIINB=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Prange C., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7T3H1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=zgc:63867;
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01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein S., Gerhard D.S.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO81081; AAH81081.1; -
InterPro, IPR006996; Dynamitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similar to dynactin 2 (P50).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7955;
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l. Acad. Sci. U.S.A.
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4 (TrEMBLrel. 26,
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403 AA; 44737
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76.7%;
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Last annotation updat
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Pred. No. 1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Schroer T.A., Gill S.R., Hasbani J., (Schroer T.A., Hasba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Role of dynactin in endocytic traffic: overexpression and colocalization with C Mol. Biol. Cell 10:4107-4120(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053120; AAH53120.1; -.
ZFIN; ZDS-GENE-040426-1279; zgc:63867.
GO; GO:0005869; C:dynactin complex; IEA.
GO; GO:000717; P:microtubule-based process; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20056093; PubMed=10588646; Valetti C., Wetzel D.M., Schrader Kreis T.B., Schroer T.A.;
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01-MAR-2003
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01-MAY-2000
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Pfam; PF04912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria; Aves; Neognathae;
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Pr04912; Dynamitin
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    DVEQIQSAVKESAAEEELTPMALARQLEGL
                                                                            EVEKIKTTVKESATEEKLTPVLLAKQLAAL 30
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Weognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                           45126 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .R., Hasbani J., Crego C.,
to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%;
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Pred. No. 0.0016;
                                                                                                                                                                 Pred. No. 0.007; Mismatches
                                                                                                                                                                                                              Score 89; I
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                                                                                                                                                                                                                                                                                                                                       F229C467C630DCB9 CRC64;
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Matches 13
Nat. Biotechnol. 22:547-553(2004).

EMBL; AB017303; AAS81104.1; -.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:Biotin carboxylase acti

GO; GO:0004075; F:biotin carboxylase acti

GO; GO:00016874; F:ligase activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR004549; AccC.

InterPro; IPR005482; Biotin carb_C.

InterPro; IPR005481; CPase_L.N.

InterPro; IPR005479; Cpbp_Symth_L.D2.

InterPro; IPR011054; Rudmnt hyb motif.

Pfam; PF02785; Biotin_carb_C; 1.
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Q874E7;
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01-JUN-2003
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Biotin Garboxylase (EC 6.3.4.14).
                                                                                                                                                                                                                                                                                                                                  PubMed=15064/bs;
Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T.,
Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias F
Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber F
Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
                                                                                                                                                                                                                                                                                                                  "The genome sequence of thermophilus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=TTC0758;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Deinococcus-Thermus; Thermus.
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PubMed=15321663; DOI=10.1016/j.femsle.2004.06.033.
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"Structures of the mating-type loci of Cordyceps takaomontana.";
Appl. Environ. Microbiol. 69:5019-5022(2003).
EMBL; AB096216; BAC67540.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22783895; PubMed=12902305; DOI=10.1128/AEM.69.8.5019-5022.2003;
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37756 MW;
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Q9LIF3;
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TIGRPAMs; TIGR00514; acCC; 1.
PROSITE; PS00866; CPSASE 1; UNKNOWN 1.
PROSITE; PS00867; CPSASE 2; UNKNOWN 1.
Complete proteome.
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28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Cytochrome P450 71B37 (EC 1.14...).
                                                                                                                                                                                                                                                                                          GeneFarm; 1244; 94.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR002401; EP450I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20363099; PubMed=10907853; Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.; "Structural analysis of Arabidoppis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 P1, T2
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PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; 1.
Heme; Monooxygenase; Multigene family; Oxidoreductase; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.1%;
                                                                                                  56843 MW;
                      39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
Score 54; DB
Pred. No. 1.6e
9; Mismatches
     9;
                                                                                                                                                                                                                                                                                                                                                                                       ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54; DB 2;
Pred. No. 1.4e+02;
2; Mismatches 8
                                                                                               Potential.
Iron (heme axial ligand)
; B36088363D918FE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions ng as its content is in
                           .6e+02
     6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
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                                             Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
     Indels
                                                                                                                      (By
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  2;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT
Q6BPD3
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Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                            InterPro; IPR004540; EF-G.
InterPro; IPR000640; EFG_CI.
InterPro; IPR000522; EFG_III_V.
InterPro; IPR005517; EFG_IV.
InterPro; IPR005517; EFTU_D2.
InterPro; IPR000795; ProtSyn_GTP)
InterPro; IPR005225; Small_GTP.
InterPro; IPR005000; TransTat_fac
                                                       PRINTS; PR00315; PR00315; PR00315; PR00315; PR00316; PR00484; EF-G; 1.
TIGREAMS; TIGR00231; Small GTP; 1.
GTP-binding; Protein biosymthesis.
GTP-binding; Protein biosymthesis.
GTP-binding; Protein biosymthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6BPD3;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Debaryomyces hansenii chromosome E of strain CBS767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                      Pfam; PF00679; EFG C; 1.
Pfam; PF03764; EFG TV; 1.
Pfam; PF00009; GTP EFTU; 1.
Pfam; PF03144; GTP EFTU D2; 1.
PRINTS; PR00315; ELONGATNECT.
                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382137; CAG88181.1; -.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0003746; F:translation elongation factor activity; IEA.
GO; GO:0003412; P:protein biosynthesis; IEA.
GO; GO:0006412; P:translational elongation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORFNames=DEHAOE15092g;
Debaryomyces hansenii (B8767.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bouchier C., Caudron B., Wincker P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genolevures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=284592;
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                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVEKIKTTVKESATEEKLTPVLLAKQLAAL
39.1%;
llarity 37.0%;
Conservative
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                                                                                                                                                                                                                              Small_GTP.
Translat_factor.
Score 54; DB Pred. No. 2.4e 6; Mismatches
 6
                                                                                                                                                                                                                                                                     _GTPbind.
                                                                       CA2EBCF93AA8EBCC CRC64;
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                  2.4e+02;
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                                    DB 2;
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                                  Length 769;
     Indels
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RESULT 14
Q6BFZ2
ID G6BFZ
AC Q6BFZ
DT 25-OC
DT 2
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GENOUT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                          25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
Hypothetical protein.
ORFNames=PTMB.230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZOBR
GLND AZOBR
QBRQD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAM8;
Nitrogen f
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                            Q6BFZ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sp7 / ATCC 29145;
Van Dommelen A., Keijers V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and characterization of the and analysis of a glnD mutant."; Mol. Gen. Genet. 266:813-820(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transferase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002912; ACT.
InterPro; IPR006674; HD hydro.
InterPro; IPR003607; Met_phos_hydro.
InterPro; IPR002934; NTP_transf.
InterPro; IPR010043; UTase_glnD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=glnD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004
Paramecium tetraurelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF149716; AAL87737.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodospirillaceae; Azospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Azospirillum brasilense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
[Protein-PII] uridylyltransferase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gen. Genet. 266:813-820(2002).
FUNCTION: Modifies, by uridylylation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (glnB) regulatory protein.
CATALYTIC ACTIVITY: UTP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the glnD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF01842; ACT; 2.
PF01966; HD; 1.
PF01909; NTP_transf_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TIGR01693; UTase glnD; 1.
fixation; Nucleotidyltransferase; Transferase.
933 AA; 104601 MW; 35E692E0411BB9E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BKIKTTVKESATEEKLTPVLLAKQLAAL
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                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Uridylyl removing enzyme) (UTase)
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                                                                                                  Created)
Last sequence
Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.8e
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [protein-PII]
                                                                                                                                                                                                                                                  PRT;
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                                                                                                      sequence update)
annotation update)
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2.7.7.59)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 933;
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Q6CF32;
25-OCT-2004
                                                                                                                                                                                                                                                        Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bespons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Strauh M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchter C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yarrowia lipolytica CLIB99.
Eukaryota; Fungi; Ascomycota; Sacc
Saccharomycetales; Dipodascaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 28, 25-OCT-2004)
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"Paramecium megabase sequencing project.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR548612; CAH03428.1; -.
InterPro; IPR001251; CRAL_TRIO_C.
PROSITE; PS50191; CRAL_TRIO; 1.
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Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
EMBL; CR382128; CAG82975.1; -.
                                                                                                                                                                                                       Zeniou
Bouchier C., Cauu.
Bouchier P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=284591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity (Fragment).
                                                                                        SEQUENCE FROM N.A.
STRAIN=CLIB99;
                                                                                                                                                                              Nature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genolevures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CLIB99;
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SEQUENCE 416 AA; 4
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Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Stock d4-2;
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                                                                                                                                                                                                          "Genome evolution in yeasts.";
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Pred. No. 1.8e+02;
6; Mismatches 10
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Maximum
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Gapop 10.0 , Gapext 0.5
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251
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Listing first 45 summaries
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score greater Pred. No. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

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45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26
64	64	64	64	64	64	64	65.5	65.5	66	66	66	66	67	67	67	67	67	67	67
25.5	25.5	25.5	25.5	25.5	25.5	25.5	26.1	26.1	26.3	26.3	26.3	26.3	26.7	26.7	26.7	26.7	26.7	26.7	26.7
188	188	188	188	188	151	140	1837	207	1020	868	386	13	2481	2481	2478	2478	2478	2478	1448
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ABU80870	AB017616	AAU12172	AAB10278	AAW64545	AAG03725	AA012168	ADS44304	AAB29754	AAM79875	AAY37731	ABU44043	ABP52977	ABR62804	ABU15838	ABM71899	ABJ19002	AAU34320	AAU37374	ADA89551
Abu80870	Abo17616	Aau12172	Aab10278	Aaw64545	Aag03725	Aao12168	Ads44304	Aab29754	Aam79875	Aay37731	Abu44043	Abp52977	Abr62804	Abu15838	Abm71899	Abj19002	Aau34320	Aau37374	Ada89551
Human PRO	•	Human PRO	Human fet	Human sto	Human sec	Human pol	Bacterial	Rice PNI-	Human pro	Protein i	Protein e	Cellular	Methicill	Protein e	Staphyloc	Pathogen	Staphyloc	Staphyloc	Staphyloc

ALIGNMENTS

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RESULT 1
ABM81421
                                                                                                                                                                                                                                                                                                         Tumour-associated antigenic target; TAT; human; overexpression; citumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                 gene therapy; cytostatic.
                                                                                                                                                                                                                                           15-APR-2004.
                                                                                                                                                                                                                                                             WO2004030615-A2
                                                                                                                                                                                                                                                                                                                                                                            Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ:3675
                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004 (first entry)
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cancer;

29-SEP-2003; 2003WO-US028547.

02-OCT-2002; 2002US-0414971P.

GENENTECH INC.

Wu ID, Zhang Z, Zhou ۲,

WPI; 2004-347921/32.

N-PSDB; ACN39497.

New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

Claim 12; SEQ ID NO 3675; 7273pp; English.

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and

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cc polypeptides; expression vectors and host cells comprising a TAT nucleic cacid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or chapmosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in the chromosome identification and in gene therapy. The present sequence
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Best Local
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19-OCT-2001;
02-NOV-2001;
09-NOV-2001;
                                                                                                Lee S, Lee BA, Lee SI, Lee Marquis JP, Ramkumar J, Rich Marquis JP, Ramkumar J, Rich Marquis J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; cerebroprotective; hypotensive; cardiant; osteo antiinflammatory; antiarthritic; virucide; gene therapy; human; structural and cytoskeleton-associated protein; SCAP; cancer; an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; antianginal; neuroprotective; cerebroprotective; hypotensive; cardiant; osteopathic;
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New human structural and for diagnosing, treating
                                                    N-PSDB; ACC44338
                                                                                                                                                     Griffin JA,
                                                                                                                                                                                             Becha SD,
                                                                                                                                                                                                                                                                                  16-NOV-2001;
07-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atherosclerosis;
                                                                      2003-403125/38
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                                                                                                                                                                         Bhatia U, B
Elliott VS,
                                                                                                                                                                                                                                                                              ; 2001US-0328931P.
; 2001US-0360681P.
; 2001US-0343896P.
; 2001US-034388P.
; 2001US-0332385P.
; 2001US-0340776P.
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                                                                                                  hatia U, Blake JJ, Borowsky ML, Burrill JD, Chang Elliott VS, Emerling BM, Forsythe IJ, Gorvad AE; Hafalia AJA, Ho A, Ison CH, Kable AE, Khare R, EA, Lee SY, Lehr-Mason PM, Li JX, Lindquist EA, Ramkumar J, Richardson TW, Sprague WW, Swarnakar rren BA, Yang J, Yue H, Zebarjadian Y, Zheng W;
                                                                                                                                                                                                                                                                2002US-0347703P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 251; DB 8
Pred. No. 6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
proteins (SCAP) useful or conditions associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                      رس, Chang H;
Gorvad AE;
S, Khare R, T
ndquir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stroke;
                                                                                                                      Lal
Luo
A;
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cytoskeleton-associated and preventing diseases

Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating the comprises detecting a modified polypeptide in a sample and correlating the comprises detecting a modified polypeptide in a sample and correlating the comprises detecting a modified polypeptide in a sample and correlating the comprises detecting a modified polypeptide in a sample and correlating the comprises detecting a modified polypeptide in a sample and correlating the comprises detecting a modified polypeptide in a sample and correlating the comprises detecting a modified polypeptide in a sample and correlating the comprises detecting a modified polypeptide in a sample and correlating the comprises detecting a modified polypeptide in a sample and correlating the comprises detecting the comprise detection and the comprise detection the comprise detection and the comprise detection and the comprise detection and the comprise detection and the comprises detection and the comprise detection and the comprises detection and the comprises detection and the comprises detection and the comprise detection and the comprises detection and the compr

correlating

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RESULT 3
ADJ69563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a novel isolated human structural and cytoskeleton-associated protein (SCAP) polypeptide. The polypeptides and polymucleotides encoding them are useful in diagnosing, treating and cypopuruleotides encoding them are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased cypopuruleotide or over expression of SCAP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's cypopuruleotide, heart (e.g. hypertension, heart failure, anginal and cypopuruleotide and associated with the expression of nucleic acid and amino acid sequences of scapenums on the expression of nucleic acid and amino acid sequences of SCAP. The SCAP or its fragments are useful in screening compounds for confictiveness as agonist or antagonist of the polypeptides, or in caltering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein profiles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                      Ghosh SS, ...
                                                                                                                                                                                                                                                                                                                                                  12-APR-2002;
17-JUN-2002;
20-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitochondrial; human; screening assay; diabetes n
Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 298; 361pp; English.
                                                                                                                                                                                                                                                                (MITO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-2003; 2003WO-US010870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteopathic; ophthalmological; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human heat mitochondrial protein as a therapeutic target SeqID1369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ69563 standard; protein; 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions, drug-target interactions, and gene expression profiles
                                                                                                                  WPI; 2003-845369/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
52; Conserv
                                                                                                                                                                                                                                                                                         MITOKOR
                                                                                                                                                                                                                                                                BUCK INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aberrant SCAP expression e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL
                                                                                                                                                                                                       Fahy
                                                                                                                                                                                                                                                                                                                                               ; 2002US-0372843P.
; 2002US-0389987P.
; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                       ED,
                                                                                                                                                                                                                                                                AGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                       Zhang
                                                                                                                                                                                                                                                                RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening assay; diabetes mellitus; osteoarthritis;
                                                                                                                                                                                              я́,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 251; DB 6;
Pred. No. 7.4e-21;
                                                                                                                                                                                                       Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                       BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer, osteoporosis,
                                                                                                                                                                                                       Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stroke; MELAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 378;
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                                                                                                                                                                                                          Glenn GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
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RESULT 4
ABP53018
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalogathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; parcoma; glioblatoma; leukaemia; lymphotid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                    21-JAN-2002; 2002WO-US001708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP53018 standard; protein; 406 AA
                                                                              New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
                                                                                                                                                         WPI; 2002-657599/70.
                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                14-FEB-2001; 2001US-00782816.
                                                                                                                                                                                                                                                                                                                                         22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                           WO200264779-A2
                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                immunologic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human p50 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP53018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1369; 180pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
                                                                                                                                                                                           Rogers GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                   disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intervention in treating a disease associated with intervention. Specifically, it refers to a method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 251; DB 7; 100.0%; Pred. No. 7.9e-21; tive 0; Mismatches 0;
                                                                                                                                                                                           Scholey JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondrial targets that
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The present invention describes an Disclosure; Fig 1; 55pp; English

isolated peptide

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comprising

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyrold, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents human p50 which is given in the exemplification of the present
Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention
                                                                                                            New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatm and diagnosis of cancer, immune disorders, cardiovascular disorders an neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 406
                                                                          Claim 11; Page 1126-1128; 1299pp;
                                                                                                                                                                                                        N-PSDB; AAF21871.
                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000WO-US005881
                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200055173-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiovascular disorder; wound healing; neurological disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multiple sclerosis; rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breast and ovarian cancer associated antigen protein sequence SEQ ID 676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB58968 standard; protein; 465
                                                                                                                                                                                                                                                                    Rosen CA, Ruben
                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                              12-MAR-1999;
                                                                                                                                                                                                                                2000-611515/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; llarity 100.0%; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 251; DB 5;
Pred. No. 8.1e-21;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arthritis; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 406;
                                                                                                                                    disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
                                                                                                                                                      treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc sequences AAF22032 - AAF22040 and AAB59129 which are used in the ci solation and characterisation of the DNA and protein sequences of the ci nvention. The breast and ovarian cancer associated DNA, protein, agonist cor antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antivital; antiallergic; hepacotropic; antidabetic; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly cortein sequences are used in the diagnosis of cancer, particularly cortein sequences are used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune corteins agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune corteins, autoimmune thyroiditis, diabetes mellitus, Crohn's consense, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; slial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
                                                                                                                                   New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
                                                                                                                                                                                                                                                                                                             14-FEB-2001; 2001US-00782816.
                                                                                                                                                                                                                                                                                                                                             21-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200264779-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cellular proliferation inhibition; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse p50 amino acid sequence SEQ ID NO:54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP53019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP53019 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious diseases
                                                                                                                                                                                                                                                                            (REGC )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunologic disorder.
                                                                                                                                                                                                           2002-657599/70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Similarity
52; Conser
                                                                                                                                                                                                                                                                            UNIV CALIFORNIA
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                                                                                                                                                                                                                                           Rogers GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; llarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                              2002WO-US001708.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                           Scholey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 251; DB 3;
Pred. No. 9.4e-21;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
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The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are th sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities

are the

Claim

2;

Page 31; 55pp;

English

present invention

describes an

isolated peptide

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comprising

immunologic

disorders.

Fig

2 55pp;

English.

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RRESULT 7
ABP53 MAP 53 MAP 54 MAP 54 MAP 55 MAP 50 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents mouse p50 which is given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cellular proliferation peptide inhibitor SEQ ID NO:51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                    Sharp
                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-2001; 2001US-00782816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP53016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP53016 standard; peptide; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and can be used as p50/dynamitin inhibitors and in
                                                                                                                                               New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
                                                                                                                                                                                                                                                                           WPI; 2002-657599/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2002; 2002WO-US001708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200264779-A2
                                                                                                                      immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lmmunologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
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                                                                                                                                                                                                                                                                                                                                Rogers GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.8%;
98.1%;
                                                                                                                                                                                                                                                                                                                                    Scholey JM,
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Pred. No. 7.1e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus"
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Best Local (
AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting callular proliferation, such as benign or mallignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, and inflammatory, angiogenic and immunologic disorders. The present sequence represents a specifically claimed peptide inhibitor of cellular proliferation from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human colon
                                                                                                                                                                                                                                                                                                                             Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-2000; 2000WO-US026524.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colorectal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           having at least 90% identity to
                                                                                                                                                                                                                                                                                                                                                                                                                                       MS,
                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colon cancer; colon cancer antigen; diagnosis; detection;
ctal carcinoma; chromosome 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                acids encoding 4277 human colon cancer-associated polypeptides, for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                       AAH35361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                       Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer antigen
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99US-0163280P.
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                                                                                                                                                                                                                                                   9803pp; English.
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98.1%;
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Pred. No. 2.8e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:6720
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ç,
                                                                                                                                                                                                                                                                                              treating
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RESULT 9
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                                                                                                                                                                                             New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to produce the colon cancer-associated Ps, by inserting the nucleic aci into a host cell and culturing the cell to express the proteins. N and can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
                                                                                                                                                                                                                                                       WPI; 2002-657599/70.
                                                                                                                                                                                                                                                                                 Sharp DJ, Rogers GC,
                                                                                                                                                                                                                                                                                                                                         14-FEB-2001; 2001US-00782816
                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2002; 2002WO-US001708
                                                                                                                                                                                                                                                                                                                                                                                                                               WO200264779-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glandular disorder; macrophagal disorder; epithelial stromal disorder; blastocoelic disorder; angiogenic
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                                                                                                                                                                                 immunologic disorders.
                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunologic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.0%; Score 231; DB 4; 100.0%; Pred. No. 4.8e-19;
                                                                                                                                                                                                                                                                                Scholey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibitor related peptide SEQ
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The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, therefore the property of the present colorectal, prostate, pancreatic, lung, vulval, therefore the present and provide the present colorectal and provide the provide the provide the provide the provided that the provided t

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Claim 1; Page 29; 55pp; English

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52969
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The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; satrocytal disorder; pypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; anglogenic disorder;
                                                                                                                                                                                                                                                Claim 1; Page 29;
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                                                                                                                                                                                                                                                                                                  leukemia
                                                                                                                                                                                                                                                                                              peptide inhibitors of p50/dynamitin useful for treating cancer by ibiting cellular proliferation, e.g. benign or malignant tumors, kemia and lymphoid malignancies, or inflammatory, angiogenic and
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100.0%;
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     The present invention describes an isolated peptide (I) comprising or CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The CC apptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and ceck tumours); leukaemias and lymphoid malignancies, other disorders such CC as neuronal, glial, astrocytal, hypothalamic and other glandular, CC macrophagal, epithelial, stromal and blastocoelic disorders; and crimmatory, angiogenic and immunologic disorders. The present sequence or carries and peptide that can be N-terminally added to (P1)
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                                                                                                                                                                                                                                                                                              Claim 1; Page
                                                                                                                                                                                                                                                                                                                               New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
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Matches Query Match

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Similarity

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Score 103; DB 5; Pred. No. 4.5e-05;

Length 20; Indels

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RESULT 12
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The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABPE2966 and ABPE2967 and can have C-terminal and N-terminal extensions. (I) have cycostatic and antiinflammatory activities and can be used as 950/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, inflammatory, angiogenic and immunologic disorders
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'note= "Leu in humans and Val in Mus musculus"
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                                              The present invention describes an isolated peptide (I) comprising or CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the Sequences given in ABP52966 and ABP52967 and can have C-terminal and N-CC terminal extensions. (I) have cytostatic and antiinflammatory activities CC peptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such CC as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such CC macrophagal, astrocytal, hypothalamic and other glandular, CC inflammatory, angiogenic and immunologic disorders. The present sequence crepresents a peptide that can be N-terminally added to (P1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 29; 55pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunologic disorders.
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Pred. No. 5.3e-05;
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                                                                                               The present invention describes an isolated peptide (I) comprising or Chaving at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the Sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and cinflammatory, angiogenic and immunologic disorders. The present sequence represents a peptide that can be N-terminally added to (P1)
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glial disorder; astrocyval disorder; hypothalamic disorder; inflammatory;
gliadular disorder; macrophagal disorder; epithelial disorder;
stromal disorder; blastocoelic disorder; angiogenic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma;
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                                                                       Sequence 18 AA;
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     llarity 100.0%; I
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                          The present invention describes an isolated peptide (I) comprising or CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The CC peptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC thyroid, hepatic carcinomas, sarcomas, glioblatcomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, CC macrophagal, epithelial, stromal and blastocoelic disorders; and crepresents a peptide that can be N-terminally added to (P1)
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                                                                                                                                                                                                                                                                                                                                            New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
Sequence 17
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SUMMARIES

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Aam78891 Human pro	Murine	Abm85826 Mouse pro	Abp56824 Human his	6 Human	Adb96563 Human his			Abu30798 Protein e	Helicoba				Aae36132 Streptomy	Abu19329 Protein e	Adb10326 Alloiococ		Abp53016 Cellular	Abp53019 Mouse p50	Breas	Abp53018 Human p50	w	Abp98851 Human str	Abm81421 Tumour-as	man	

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat discorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P

Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.

Claim 11; Page 8181; 9803pp; English.

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Adq19111	Abu29933	Abg42023	Abg53895	Aam59635	Aam72208	Aam32468	Abb38983	Adr99164	Adq39510	Adq39509	Adj75521	Adn95526	Add48597	Adj70171	Adp23738	Adn04531	Adq39515	Adq39513	***************************************
Human sof	Protein e	Human pep	Human liv	Human bra	Human bon	Peptide #	Peptide #	Chondroit	Human myo	Human myo	Marker ge	Human BEC	Human Pro	Human hea	PRO polyp	Antipsori	Human myo	Human myc	Total statement

ALIGNMENTS

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RESULT 1
AAG75956
03-SEP-2001 (first entry)
                                                                                                                                   N-PSDB; AAH35361.
                                                                                                                                           WPI; 2001-235357/24.
                                                                                                                                                          Ruben SM, Barash SC,
                                                                                                                                                                                         29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                               28-SEP-2000; 2000WO-US026524
                                                                                                                                                                                                                               05-APR-2001.
                                                                                                                                                                                                                                             WO200122920-A2.
                                                                                                                                                                                                                                                                          Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 12.
                                                                                                                                                                                                                                                                                                Human colon cancer antigen protein SEQ ID NO:6720.
                                                                                                                                                                                                                                                                                                                               AAG75956;
                                                                                                                                                                                                                                                                                                                                              AAG75956 standard; protein; 134
                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
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99US-0163280P.
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                        mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour-associated antigenic target; TAT; human; overexpression; citumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                              The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2002;
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treating a cell

proliferative

disorder associated

This sequence represents a novel isolated human structural and cytoskeleton-associated protein (SCAP) polypeptide. The polype

encoding

them

are useful

polypeptide. The ul in diagnosing,

treating polypeptides

and

Claim 1;

Page 298; 361pp; English.

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RESULT 3
ABP98851
ID ABP9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; cerebroprotective; hypotensive; cardiant; ostec
antiinflammatory; antiarthritic; virucide; gene therapy; human;
structural and cytoskeleton-associated protein; SCAP; cancer; ar
atherosclerosis; epilepsy; Huntington's disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 314 AA;
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07-DEC-2001;
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09-NOV-2001;
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                                                                                                                                             human structural and cytoskeleton-associated proteins (SCAP) useful diagnosing, treating and preventing diseases or conditions associated the aberrant SCAP expression e.g. cancer, osteoporosis, or epilepsy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVEKIKTTVKESATEEKLTPVLLAKQLAAL
                                                                                                                                                                                                                                                                                                                                                                       Bhatia U, Blake, Elliott VS, Er A, Hafalia AJA, ee EA, Lee SY, !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
ilarity 100.0%;
Conservative (
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2001US-0343896P.
2001US-0346308P.
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2001US-0340776P.
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                                                                                                                                                                                                                                                                                                                                                Ramkumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002US-0347703P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0328931P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoporosis; osteoarthritis.
                                                                                                                                                                                                                                                                                                                              BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and cytoskeletal associated
                                                                                                                                                                                                                                                                                          Blake JJ, Borowsky ...,
/S, Emerling BM, Forsythe IJ, Gorvau ...,
/AJA, Ho A, Ison CH, Kable AE, Khare R,
SY, Lehr-Mason PM, Li JX, Lindquist EA,
SY, Lehr-Mason TW, Sprague WW, Swarnaka:
'I' J, Richardson TW, Zebarjadian Y, Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 particularly cancers such as breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 138; DB 8;
Pred. No. 3.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anticonvulsant; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein #42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                            Swarnakar
Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteopathic;
uman; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Η,
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RESULT 4
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preventing diseases or conditions associated with the decreased expression or over expression of SCAP, such as cell proliferative (e.g. expression or over expression of SCAP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), heart (e.g. hypertension, heart failure, angina) and skeletal muscle disorders (e.g. osteoporosis, osteoarthritis) or viral infections. These are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of SCAP. The SCAP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions described the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitochondrial; human;
Huntington's disease;
Leber's hereditary opt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                  Identifying a mitochondrial target for drug screening assays and treating diseases associated with altered mitochondrial function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-2003; 2003WO-US010870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human heat mitochondrial protein as a therapeutic target SeqID1369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ghosh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MITO-) MITOKOR (BUCK-) BUCK IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interactions, drug-target interactions, and gene expression profiles
                                                                                                                                                                                                                                                                                                                                                                                                                ካ SS,
≮ DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fahy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening assay; diabetes mellitus;
osteoarthritis;
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Pred. No. 3.9e-11;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibson BW, Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽
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                                                                                                                                                                                                                                                                                             assays and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glenn
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comprises detecting a modified polypeptide with the disease.

in a

sample

and

correlating

Disclosure;

Fig 1; 55pp;

English.

This invention relates to novel for therapeutic intervention in altered mitochondrial function.

mitochondrial targets that can be used treating a disease associated with specifically, it refers to a method fo

a method for

The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (PI) or (P2). Where (PI) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast,

Claim 1;

SEQ

ID NO 1369; 180pp;

English

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RESULT 5
ABPS3018
ID ABPS
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XX ABPS
XX ABPS
XX ABPS
XX ABPS
XX OS-N
XX Cell
XW P50
XW Glia
XW Gl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-657599/70.
                                                                                                                                                                                                                                                                                                                               New peptide inhibitors of p50/dynamitin useful for treating cancer linhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sharp DJ, Rogers GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-2001; 2001US-00782816
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30; Conserv
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ilarity 100.0%;
Conservative 0
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Pred. No. '
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                        Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; noticinglammatory; antivicer; vulnerary, anticonvulsant; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and bhastocoelic disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents human p50 which is given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                            Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                           neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment diagnosis of cancer, immune disorders, cardiovascular disorders as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-2000;
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Pred. No. 4.3e-11;
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cer; vulnerary; anticonvulsant;
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p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; satrocome; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder; Mus musculus. 22-AUG-2002 WO200264779-A2 immunologic disorder.

21-JAN-2002; 2002WO-US001708

14-FEB-2001; 2001US-00782816

(REGC) UNIV CALIFORNIA

Ď, Rogers GC, Scholey JM;

New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders. γd

Fig 55pp; English.

The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such

antifungal; antiparasitic

and cardiant

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RESULT 8
ABP53016
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macrophagal, epitl
inflammatory, ang
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The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, such as benign or malignant tumours (renal, liver, kidney, bladder, breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; ps0 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; ps1 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; ps2 inhibitoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
                                                                                                                                                              New peptide inhibitors of p50/dynamitin useful for thinhibiting cellular proliferation, e.g. benign or malleukemia and lymphoid malignancies, or inflammatory, immunologic disorders.
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                                                                                                                                      2; Page 31; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                              2002WO-US001708
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1; Mismatches
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                                                                                                                                                                                                                           New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
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stromal disorder; blastocoelic disorder;
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The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (PI) or (P2). Where (PI) and (P2) are th sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities

Claim 1;

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English

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be used as p50/dynamitin inhibitors

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The present invention describes an isolated polynucleotide (I) of Alloiococcus ottitidis genomic DNA, which encodes an antigenic protein. Alloiococcus ottitidis is a Gram-positive bacterium. Also described: (1) an isolated polypeptide that is encoded by the polynucleotide (I); (2) an expression vector comprising the novel isolated polynucleotide (I), its complement, degenerate variant or fragment; (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2); (4) an antibody specific for the polypeptide of (I); (5) an immunogenic composition comprising the polypeptide of (I); (5) an immunogenic equivalent or fragment, or the polypeptide that is comprised in the polypeptide of (1) and a carrier; (7) a protein chip comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) immunising against Alloiococcus otitidis by administering to a host the immunising against Alloiococcus otitidis by administering to a host the
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18-NOV-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4734; 1019pp; English.
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2002US-0426742P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clinical trials.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigenic protein; immunogenic;
itive bacterium; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334
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Pred. No. 1.5e-07;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Russell DP, Zagursky RJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for demonstrates with monitoring
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composition;

(9)

detecting

and/or

Alloiococcus

the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 47253; 1766pp; English.

invention relates to an isolated nucleic acid comprising any one of

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ABULT 11
ABU19329
ID ABU19329
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Ant
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Best Local
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing the novel polynucleotide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the genetically engineered host cell under conditions suitable to produce the polypeptide from the culture. (I) can be used in gene therapy. The polynucleotides, polypeptides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials. The polynucleotides are useful for expressing and detecting Alloiococcus otitidis. The present sequence represents an Alloiococcus otitidis antigen protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-029926/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           otitidis in the biological sample; (10) a kit comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-)
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Trawick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Carr G
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34.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ີດ <sup>(</sup>ບ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               essential gene #4856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen
Forsyth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a container
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zyskind JW;
Xu HH;
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CC proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) CC identifying a gene required for cellular proliferation or the biological CC pathway in which a proliferation-required gene or its gene product lies CC or a gene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent CC which each of the strains is present in a culture or collection of CC strains; or (13) identifying the target of a compound that inhibits the CC proliferation of an organism. The antisense nucleic acids required CC drug discovery programs, or for screening for homologous nucleic acids required CC drug discovery programs, or for screening homologous nucleic acids could discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, CC the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained CC in electronic format directly from WIPO at CC fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 11
Novel cytochrome P450 enzyme and nucleotides encoding the enzyme, use for preparing amphotericin derivative or analog antibiotic agent with altered properties, in biosynthesis of polyketide other than
                                                                                                                            N-PSDB; AAD54645.
                                                                                                                                                            WPI; 2003-201271/19.
                                                                                                                                                                                                                       Caffrey
                                                                                                                                                                                                                                                                                                                                                31-MAY-2001; 20011E-00000527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces nodosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polyene; antibiotic;
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                                                                                                                                                                                                                                                                                     AIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amphotericin; amph; polyketide synthase; enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene encoded protein.
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Pred. No. 2.9e+02;
6; Mismatches 12
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The invention relates to the gene cluster encoding the polypeptides responsible for the biosynthesis of the polypene antibiotic amphoteric (amph) of Streptomyces nodosus. Polypucleotides of the invention are useful for preparing amphotericin derivatives or analogue antibiotic

amphotericin

Claim 6; Page 227-276;

276pp;

English

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RESULT 13
AAG61007
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                                               06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
                                                                                                 28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agents with altered properties and in the biosynthesis of polyketides other than amphotericin. amphDIII, amphDII or amphDI mutants are useful for producing amphotericin derivatives glycosylated with alternative sugars; amphDIII or amphDII gene sequences are useful in engineered biosynthesis of perosaminyl-amphoteronolide B; amphDIII or amphDII and amphN gene sequences are useful in the engineered biosynthesis of perosaminyl-16-methyl amphoteronolide B; amphDIII, amphDII and amphNI gene sequences are useful for preparing polypeptides capable of addition of mycosamine to a polyketide other than amphoteronolide A or B or for preparing polypeptides for in vitro synthesis of GDP-mycosamine. The present sequence is polyketide synthase multienzyme housing extension modules 3, 4, 5, 6, 7 and 8 encoded by S. nodosus amphC gene
                                                                                                                                                                  23
                                                                                                                                                                                                                                            01-APR-1999;
06-APR-1999;
            14-MAY-1999;
14-MAY-1999;
                                      14-MAY-1999;
                                                                                                                                                                                                                                 08-APR-1999
                                                                                                                                                                                                                                                                                                              09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification, signal transduction hybridisation assay; genetic mapping; gene (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ
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                                                                                                                                                                                                       19-APR-1999;
                                                                                                                                                                                                                     16-APR-1999
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                                                                                                                                                                                                                                                                                    25-MAR-1999
                                                                                                                                                                                                                                                                                                                                     25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      termination
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mapping; gene expression control; promoter;
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174 EPERVKTMIEEFLTEEKI 191
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nilarity 50.0%;
Conservative
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promoter;
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05-AUG-1999
9905-014712029
06-AUG-1999
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ID 187016
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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: CC (1) a vector comprising a promoter operably linked to the nucleic acid CC encoding a polypeptide whose expression is inhibited by the antisense CC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for CC proliferation, (7) identifying a compound that influences the activity of identifying a gene product or that has an activity against a biological pathway required for required for relular proliferation, (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation, or that inhibits cellular proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene CC or a gene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene CC product is overexpressed or underexpressed; (12) determining the extent CC to which each of the strains is present in a culture or collection of collection of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to late candidate molecules for rational drug discovery programs.
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DB; ACA20637.
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CC for cellular proliferation to isolate candidate molecules for rational CC drug discovery programs, or for screening homologous nucleic acids CC required for proliferation in cells other than S. aureus, S. typhimurium, CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this CC in electronic format directly from MIPO at CC ftp.wipo.int/pub/published_pct_sequences

XX XX XX XX Sequence 640 AA;

Query Match
Best Local Similarity 39.3%; Pred. No. 2.6e+02;
Matches 11; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 3 EKIKTTVKESATEEKLTPVLLAKQLAAL 30

QY 3 EKIKTTVKESATEEKLTPVLLAKQLAAL 30

131 DKYQKLVKEKASDEEITQHLMLPMLRAL 158

Search completed: November 3, 2005, 21:57:27

Job time: 44.0695 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.
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A;Gene: gyrB C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain	C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_cna C;Accession: B71931 R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.; Ives, C.; Gibson, R.; Mexberg, D.; Mills, S.D.; Jiang, Q.; Nature 397, 176-180, 1999 A;Title: Genomic sequence comparison of two unrelated isolat A;Reference number: A71800; MUID:99120557; PMID:9923682 A;Accession: B71931 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-773 <arn's a;cross-references:="" a;experimental="" c;genetics:<="" gb:ae001439="" gb:ae001479;="" j99="" source:="" strain="" th="" uniprot:q9zlx3;=""><th>VRESATEEKLIPVILLA 24 :: : :: : :: : :: </th><th>38.4%; Score 53; DB 2; Similarity 40.9%; Pred. No. 67; 9; Conservative 7; Mismatches 6</th><th>A;Status: preliminary; translated from GH/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1394 <gei> A;Cross-references: UNIPROT:O01787; EMBL:AF003136; PII A;Experimental source: strain Bristol N2; clone F28B3 C;Genetics: A;Gene: CESP:F28B3.1 A;Map position: 1 A;Introns: 46/3; 105/2; 280/3; 337/1; 358/1; 530/3; 68</gei></th><th>.; Smith, A. ata Library, May ata Library, May ence of C. elega</th><th>n F28B3.1 - Caeno bditis elegans #sequence_revisi</th><th>46 33.3 757 1 46 33.3 757 2 46 33.3 1103 2 46 33.3 1612 2 46 33.3 2254 2 45.5 33.0 253 2 45.5 33.0 253 2</th><th>66 33.3 482 2 66 33.3 554 2 66 33.3 560 2 66 33.3 574 2 66 33.3 710 2 66 33.3 727 2</th><th>46 33.3 124 2 46 33.3 190 2 46 33.3 205 2</th></arn's>	VRESATEEKLIPVILLA 24 :: : :: : :: : ::	38.4%; Score 53; DB 2; Similarity 40.9%; Pred. No. 67; 9; Conservative 7; Mismatches 6	A;Status: preliminary; translated from GH/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1394 <gei> A;Cross-references: UNIPROT:O01787; EMBL:AF003136; PII A;Experimental source: strain Bristol N2; clone F28B3 C;Genetics: A;Gene: CESP:F28B3.1 A;Map position: 1 A;Introns: 46/3; 105/2; 280/3; 337/1; 358/1; 530/3; 68</gei>	.; Smith, A. ata Library, May ata Library, May ence of C. elega	n F28B3.1 - Caeno bditis elegans #sequence_revisi	46 33.3 757 1 46 33.3 757 2 46 33.3 1103 2 46 33.3 1612 2 46 33.3 2254 2 45.5 33.0 253 2 45.5 33.0 253 2	66 33.3 482 2 66 33.3 554 2 66 33.3 560 2 66 33.3 574 2 66 33.3 710 2 66 33.3 727 2	46 33.3 124 2 46 33.3 190 2 46 33.3 205 2
1 B	<pre>wm, E.D.; Doig, P.C.; Smith, D.R.; g, Q.; Taylor, D.B.; Vovis, G.F.; isolates of the human gastric path 2</pre>		Length 1394; ; Indels 0; Gaps 0;	PIDN:AAB93633.1; GSPDB:GN00019; CESP: B3		:_change 09-Jul-2004	secretory componen polymeric immunogl Ca2+-transporting probable peptidogl protein TGD22.14 [histone H1.4 - Cae protein C18G1.5 [i	signal recognition hypothetical prote protein YKR029c ho CLB1-like protein DNA topoisomerase hypothetical prote	hypothetical prote protein F59A7.4 [i phosphoprotein pho

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th, T.; Connetcon, P.
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Authors: Complete genome sequence of a multiple drug resistant
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: AB0502; MUID:21534947; PMID:11677608
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
Nature 390, 580-586, 1997
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A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: C70191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 penicillin-binding protein (pbp-3) homolog - Lyme disease spirochete C;Species: Borrella burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004 C;Accession: C70191
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A;Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipoate-protein ligase B (lipoate biosynthesis protein B) [imported] - Salmonella C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-932 <KLE>
                                         RESULT 5
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Superfamily:
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At2g11890 [imported]
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                 A; Cross-references: EMBL: AL117455
A; Experimental source: adult uterus;
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y., M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, I euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 388, 539-547, 1997

Arauthors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; A; Title: The complete genome sequence of the gastric pathogen Helicobacter pyla; Reference number: A64520; MUID:97394467; PMID:9252185

A; Accession: E64582
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: E64582
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-200
C;Accession: E84499
                                                                                                                                                                             hypothetical protein DKFZp586J0917.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17245
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A; Residues: 1-73 < TOM>
A; Residues: 1-73 < TOM>
A; Cross-references: UNIPROT: P55992; GB: AE000564; GB: AE000511;
C; Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
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A;Map position: 2
C;Superfamily: uncharacterized
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A;Molecule type: DNA
A;Residues: 1-210 <STO>
A; Molecule type: mRNA
A; Residues: 1-878 < KOE>
                                                     A;Status: preliminary
                                                                          A; Accession: T17245
                                                                                                     A; Reference number: Z18722
                                                                                                                               R; Koehrer, K.; Beyer, A.;
submitted to the Protein
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                                                                                                                                                          A.; Mewes, H.W.; Gassenhuber,
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clone DKFZp586J0917

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A,Cross-references: UNIPROT:O9PDZ4; GB:AE003957; GB:AE003849; NID:g9106207; PIDN:AAF8404
A,Experimental source: strain 9a5c
R;Simpson, A.J.G; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajiana, J.P.; Krieger, J.B.; Kuramae, E.B.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, F.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaka
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2

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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG1717
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche,
R;Glaser, P.; Frangeul, L.; Buchaud, E.; Durand, L.; Dussurget, O.; Entian, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 bel
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; A; Authors: Kreft, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; ok, C.; Schlueter, T.; Sensonics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1717
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A;Experimental source: strain Clip11262
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A; Residues: 1-1151 <GLA>
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A;Residues: 1-298 <SIM>
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44.0%;
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Pred. No. 1.4e+02;
4; Mismatches 3;
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Pred. No. 1e+0
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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Voss, H.; W
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Faihi, H.
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primosome component (helicase loader) dnaI - Bacillus subtilis N; Alternate names: dnaA protein homolog, 44K; hypothetical pro
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A;Cross-references: UNIPROT:084720; GB:AE001342; GB:AE001273; NID:g3329166; PIDN:AAC6831
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
                                                                                                                                                                                                                                                                                    RiStephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: B71480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Contents: annotation C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004 C;Accession: B71480
                                                                                                                                                                                                                                                                                                                                                                                                                             probable agx-1 homolog-udp-glucose pyrophosphorylase - Chlamydia trachomatis (serotype \Gamma C;Species: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: XF1234 C;Superfamily: carboxyphosphonoenolpyruvate phosphonomutase
                                                                                                                                                    A;Gene:
                                                                                                                                                                                                                                                                  A;Status: preliminary
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A;Cross-references: UNIPROT:Q96MK3; EMBL:AL133105
A;Experimental source: adult testis; clone DKFZp4
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A; Accession: T42684
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C;Species: Homo
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                                                                         Matches
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Best Local
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Best Local Similarity
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                                                                                                                                                    CT715
264
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omo sapiens (man)
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                                                                     Score 49; DB
Pred. No. 70;
6; Mismatches
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Pred. No. 51;
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protein

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A;Molecule type: DNA
A;Residues: 1-18,'N', 20-23,'T', 25-206 <HOS>
A;Residues: 1-18,'N', 20-23,'T', 25-206 <HOS>
R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A; Bhrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.
A; Authors: Soulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Massada, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Title: The complete genome sequence of the Gram-postiive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69617
A.;Ceassion: F69617
A; Molecule type: mRNA
A; Residues: 1-211 < KAT'>
A; Cross-references: UNIPROT: Q9SLT'9; EMBL: AB028229; PIDN: BAA87954.1
A; Experimental source: cultivar Columbia
C; Genetics:
C; Genetics:
A; Map position: 1
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F;168-175/Region:
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C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: B24720; C25580; F69617
R;Ogasawara, N.; Moriya, S.; Mazza, P.G.; Yoshikawa, H.
Nucleic Acids Res. 14, 9989-9999, 1986
A;Title: Nucleotide sequence and organization of dnaB gene and neighbouring genes on the A;Reference number: A93650; MUID:87117549; PMID:3027671
A;Accession: B24720
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A; Residues: 1-311 < CGA>
A; Residues: 1-311 < CGA>
A; CRESICUES: FEFERENCES: UNIPROT: P06567; GB: X04963; NID: g39880; PIDN: CAA28633.1; PID: g39881
A; Cross-references: UNIPROT: P06567; GB: X04963; NID: g39880; PIDN: CAA28633.1; PID: g39881
R; Hoshino, T.; McKenzie, T.; Schmidt, S.; Tanaka, T.; Sueoka, N.
Proc. Natl. Acad. Sci. U.S.A. 84, 653-657, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 653-657, 1987
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A,Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14858.1; PID:g2635363
A,Experimental source: strain 168
                                                                                                                                                                                                                                                     A;Reference number: Z25171
A;Accession: T52431
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                 Gene 239, 309-316, 1999
A;Title: Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                               R;Kato, A.; Suzuki, M.; Kuwahara, A.; Ooe, H.; Higano-Inaba, K.; Komeda, Y. Gene 239, 309-316, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ZCF37 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
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A;Reference number: A94709; MUID:87118226; PMID:3027697
A;Accession: C26580
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Pred. No. 54
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R;Johnson, D.
submitted to the EMBL Data Library, June 1995
submitted to the EMBL Oata Library, June 1995
A;Description: The sequence of C. elegans cosmid C17G10
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                                                                                                                                                                                                                                                                                                                                                                                      cell division control protein. PAB2373 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CESP:C17G10.2
A;Map position: 2
A;Introns: 36/3; 81/1; 167/1; 252/3; 355/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-379 <JOH>
A;Residues: 1-379 <JOH>
A;Cross-references: UNIPROT:Q09974; EMBL:U28739; PIDN:AAB93452.1; GSPDB:GN00020; CESP:C1
A;Experimental source: strain Bristol N2; clone C17G10
C;Genetics:
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A; Residues: 1-1112 <KAW>
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                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                          Dynactin complex 50 (p50 dynamitin) (DCT 23-48K) (GMP23-48K).
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                                                                                              musculus (Mouse)
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an email to license@isb-sib.ch).
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als M., Martens L., Van Damme J., Sta
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E -> ELE (in Ref. 3).
LATV -> PGHS (in Ref. 3).
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                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 4.7e-17;
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                                                                                                                                                                dynein-associated (Growth cone membra
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RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Fahey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., RA Blakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human T and mouse cDMA secuences."
DOMAIN
SEQUENCE
                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoogenraad C.C., Akhmanova A., Howell S.A., Dortland B.R., de Zeeuw C.I., Willemsen R., Visser P., Grosveld F., Galjart N., "Mammalian Golgi-associated Bicaudal-D2 functions in the dynein-dynactin pathway by interacting with these complexes.";
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97289622; PubMed=9144527; DOI=10.1006/bbrc.1997.6447; Abe T.K., Tanaka H., Iwanaga T., Odani S., Kuwano R.; "The presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the 50-kDa subunit of dynactin complex in the presence of the base of
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SUBCELLULAR LOCATION,
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                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH BICD2.
MEDLINE=21376052; PubMed=11483508; DOI=10.1093/emboj/20.15.4041;
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growth cone."
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                                                                                                                                                                                                                                                 MGD; MGI:107733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Subunit of dynactin, a multiprotein complex associated with dynein (By similarity). Interacts with BICD2.
SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic and membrane-associated forms in neonates. Levels of membrane-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Modulates cytoplasmic dynein binding to an organelle, and plays a role in prometaphase chromosome alignment and spindle organization during mitosis. May play a role in synapse formation during brain development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated form are greatly reduced in the adult.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                         PF04912; Dynamitin; 1.
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                                                                                                                                                         coil;
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                                                                                                                           il; Cytoskeleton; Direct protein sequencing;
Microtubule; Motor protein.
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DEVELOPMENTAL STAGE.
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By similarity.

Coiled coil (Potential).

Coiled coil (Potential).
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Query Match Best Local Matches 5

Similarity

98.8%; 98.1%;

Score 248; Pred. No. 9

DB 1; .4e-17;

Length 401;

Indels

0;

Gaps

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Mismatches

Conservative

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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.;
A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Scheetz T.E.,
A Hopkins R.F., Jordan N.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Hopkins R.F., Jouellan R., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Holton S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Touchman J.W., Green B.D., Dickson M.C.,
A Morley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S. T. Warra M. A.
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Best Local S
Matches 51
                                                                                Q6IRB3;
Q6IRB3;
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Q6AYH5;
                       Dctn2-prov protein.
Name=dctn2-prov;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC079042; AAH79042.1; -. GO: GO:005869; C:dynactin complex; IEA. GO: GO:0007017; P:microtubule-based process; IEA. InterPro; IPR006996; Dynamitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=12477932; DOI=10.1073/pnas.242603899;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF04912; Dynamitin; SEQUENCE 402 AA; 44148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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(TrEMBLrel.
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(African clawed frog)
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28,
                                                                                   Last sequence update)
                                                                                                                                         Created)
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Pred. No. 9.4e-17;
1; Mismatches 0
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Schnerch A., Schein J.E.,
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RESULT 5
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Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max, Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max, Rubin G.M., Hong L.,

Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Richards S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hoskiey R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

Jones S.J., Marra M.A.,

"Gener S.J., Marra M.A.,

"G
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                                                                                                                                                                                                                        Q66J30;
25-OCT-2004
25-OCT-2004
25-OCT-2004
MGC82128 pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S., Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ day
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ day
EMBL, BC070987; AAH70987.1; -.
GO; GO:0005869; C:dynactin complex; IEA.
GO; GO:0007017; P:microtubule-based process; IEA
                                                            Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrzehia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                              MGC82128 protein.
Name=MGC82128;
                                                                                                                                                                                                                                                                                                                                                                           Q66J30
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44828 MW;
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84.6%;
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Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                                                                                                              403
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                                                                                             Pipoidea;
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RESULT 6
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ID Q7ZX
AC Q7ZX
AC Q7ZX
AC Q7ZX
AC Q7ZX
AC Q7ZX
DT 01-J
DT 01-C
DE DCtr
OS Xenc
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RRA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RRA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RRA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RRA Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RRA Diatchenko L., Marusina K.J., Sonaldo M.F., Casavant T.L., Scheetz T.E.,
RRA Diatchenko L., Marusina K.J., Toshiyuki S., Carninci P., Prange C.,
RRA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RRA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RRA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RRA Robesk S.A., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RRA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RRA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RRA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RRA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RRA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RRA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
RRA Arnes S. J. Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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Q7ZXY2;
01-JUN-2003
01-JUN-2003
   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                         TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Crania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S.L., Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22341132;
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TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                   Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -JUN-2003 (TrEMBLrel. 24,
-JUN-2003 (TrEMBLrel. 24,
-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                _TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S., Gerhard D.S.;
tted (AUG-2004) to the EMBL/GenBank/DDBJ
BC081081, AAH81081.1; -.
Pro; IPR006996; Dynamitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ή.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
                                                                                                                                                                                                                          FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMKETPQQKYQRLLHEVQELTQEVEKTQSTVKESAAEEKLTPVALAKQVASL 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225:384-391 (2002)
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                                                                                                                                                                                                                                                                                                                Xenopus.
                                                                                                                                                                                                                          N.A.
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AA; 44737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=12454917; DOI=10.1002/dvdy.10174; Bberg R.L., Wagner L., Pontius J., Clifton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44737 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.9%;
82.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                    Mesobatrachia;
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Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length 403;
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Best Local (
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                                                                                                                                                                               Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC044069; AAH44069.1; -.
GO; GO:0005869; C:dynactin complex; IEA.
GO; GO:0007017; P:microtubule-based process; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                  SEQUENCE
                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                     Richardson P.
                                                                                                                                                                                                                                                                                                                                                                                 Klein S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      initiative.
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                Genetic and genomic tools
                                                                                                                                                                                                                                                                   :SSUE=Embryo;
                                                                                                                               Pro; IPR006996; Dynamitin.
PF04912; Dynamitin; 1.
NCE 338 AA; 38257 MW;
   31
                                                                 43;
                                  w
                                                                                  Similarity
                    KETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
KETPQQKYQRLLHEVQELTQEVEKTQSTLKESATEEKLTPVALAKQVAAL
                                                                                                                                                                                                                                                                                                                   225:384-391 (2002).
                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.L.,
                                                                  Conservative
                                                                                84.1%;
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                                                                  4.
                                                                 Score 211; DB 2
Pred. No. 4e-13;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Wagner L.,
                                                                                                                                                                                                                                                                                                                                                    Xenopus research: The NIH Xenopus
                                                                                                                                    3346E0F0F644B186 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Pontius J., Clifton S.W.,
                                                                                                 2;
                                                                  ω,
                                                                                                Length 338;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  full-length human
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Prange C.,
Mullahy S.J.,
     80
                                  52
                                                                  0
                                                                 Gaps
                                                                    0;
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RESULT 7
Q9PTG6
ID Q9PT DR REPERED RANGE Q9PTG6; 01-MAY-2000 01-MAY-2000 01-MAR-2003 Schroer T.A., Gill S.R., Ha Submitted (NOV-1999) to the EMBL; AF200744; AAF13996.1; GO; GO:0005869; C:dynactin SEQUENCE FROM N.A.
SCHOOL T.A., Gill S.R., Hasbani J., Crego C.,
Schroer T.A., Gill S.R., Hasbani J., Crego C.,
Livead (NOV-1999) to the EMBL/GenBank/DDBJ WEDLINE=2005693; PubMed=10588646; Valetti C., Wetzel D.M., Schrader M., H Kreis T.E., Schroer T.A.; "Role of dynactin in endocytic traffic: overexpression and colocalization with Mol. Biol. Cell 10:4107-4120(1999). Eukaryota; Metazoa; Chordata; Archosauria; Aves; Neognathae; Gallus gallus (Chicken). Dynamitin. Q9PTG6 SEQUENCE FROM N.A. NCBI_TaxID=9031; (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. PRELIMINARY; Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani 13, 13, 23, Last Last annotation Created) sequence update) M., Hasbani M.J., 402 : effects of CLIP-170."; B update) dynamitin Gill S. Phasianinae;

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RESULT OTTSHIT ID OTTSHIT OTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K.J., Max, Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A..
                                                                                                              Query Match
Best Local S
Matches 35
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                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNames=zgc:63867;
Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similar to dynactin 2 (P50).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.;
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Pfam; PF04912;
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                                                                                                                                                                                                                                                                               InterPro; IPR006996; Dynamitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                          GO:0005869; C:dynactin complex; IEA. GO:0007017; P:microtubule-based process;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA
                                                                                                                                                                                                                                                                                                                                                               tted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
BC053120; AAH53120.1; -.
ZDB-GENE-040426-1279; zgc:63867.
  96
                                                                                                                                                                                                                                                          PF04912;
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                                                                                                              35;
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                             GVKETPQQKYQRLLHEVQELITEVEKIKTTVKESATEEKLTPVLLAKQLAAL
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GVKETPÖÖKYÖRLVNEIHELCODVEKIÖTSTKESGAEERLTPVALAQQAAQL 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 AA; 45126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and initial analysis of more than 15,000
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                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences.";
                                                                                                                                                                                                                            Dynamitin; 1.
AA; 44625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                      70.5%;
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Pred. No. 1.2e
8; Mismatches
                                                                                                              8;
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                                                                                                        Score 177; DB 2; I
Pred. No. 1.2e-09;
8; Mismatches 9;
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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                                                                                                                                                                                                                         CA00047342500953 CRC64;
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No. 1.2e-09;
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RESULT 9

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschil S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Histing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Kones S. T. Mayra M.A.
                                                                                                                             Matches
                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                     Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC072065; AAH72065.1; ...
GO; GO:0005874; C:microtubule; IEA.
GO; GO:0000226; P:microtubule cytoskeleton organization and b.
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                       InterPro; IPR000435; Tektin.
Pfam; PF03148; Tektin; 1.
PRINTS; PR00511; TEKTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=MGC78949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dev. Dyn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
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336
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                                                           12
                                                                                                                                                             Similarity
RLINEVQEITTNIERLRETLSQAETELK 363
                                                           RLLHEVQELTTEVEKIKTTVKESATEEK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225:384-391 (2002) .
                                                                                                                                                                                                                                                              402 AA;
                                                                                                                             Conservative
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                                                                                                                                                         46.48;
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Last sequence update)
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                                                                                                                                                         Score 76; DB
Pred. No. 16;
                                                                                                                             Mismatches
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RESULT 10 Q9V4Y9 ID Q9V4Y

Q9V4Y9

PRELIMINARY;

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PRINGER BORGER BERGER B
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RA Adams M.D., Calniker S.E., Hichards S., Asbburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.H., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Blazer B.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dowles S.,
RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferriera S., Chandra I.,
RA Glodek A., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Walshin R., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravizz S., Kull D., Lai Z.,
Liang Y., Lin X.,
RA Harlis N.L., Moharry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siapen M., Shupshi M.P., Smith T.,
RA Shue B.C., Stapleton M., Shupshi M.P., Smith T.,
RA Shue B.C., Stapleton M., Shupshi M.P., Smith T.,
RA Shue B.C., Shan M., Shupshi M.P.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CG8269-PA (LD07994p).
Name=Dmn; ORFNames=CG8269;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                      Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";

Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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01-MAY-2000
                                                                                                 MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronm.
Patel S., Frise E., Wheeler D.A.,
Ashburner M., Celniker S.E.;
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                            "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22426065;
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3:RESEARCH0084-RESEARCH0084 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=12537568;
                                                                                                                                    Kronmiller D.A., Lewis
                                                                                                                                 S.E., C
                                                                                                                                                                 Carlson
                                                                                                                                        Rubin
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Best Local
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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MEDLINE=22426069; PubMed=12537572;

MISTATINE=22426069; PubMed=12537572;

MISTATINE=22426069; PubMed=12537572;

MISTATINE=22426069; PubMed=12537572;

MISTATINE B.H., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.I.

Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B

Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF04912; Dyna;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IntAct; Q9V4Y9;
FlyBase; FBgn00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Brokstein P., Hong L., Agbay Champe M., Chavez C., Dorsett V., Farfan I Gonzalez M., Guarin H., Li P., Liao G., M. Nunco J., Pacleb J., Paragas V., Park S., Yu C., Lewis S.E., Rubin G.M., Celniker S.
German Neurospora genome project;
Submitted (NOV-2003) to the EMBL/G
EMBL; BX842625; CAE76249.1; -.
GO; GO:0005525; F:GTP binding; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005869; C:dynactin complex; GO; GO:0007017; P:microtubule-based InterPro; IPR006996; Dynamitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY061092; AAL28640.1; -.
Intact: Oquavo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AE003835; AAF59034.1; -.
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                    Nyakatura
                                                                                                                                                                                          Schulte
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                       NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; I
Sordariomycetidae;
                                                                                                                                                                                                                                                                                                                                   Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                 Probable translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lewis S.E.;
                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                         Name=B16D18.090;
                                                                                                                                                   e U.,
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                                                                                     FROM N.A.

U., Aign V., Hoheisel U., --
ra G., Mewes H.W., Mannhaupt G.;
ra G., Mewes H.W., Mannhaupt G.;
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                                                                                                                                                                                                                                                                                    Ascomycota; Pezizomycotina; Sordariales; Sordariaceae;
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48.7%;
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Last annotation updat
tion factor EF-G, mitc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72.5; DI
Pred. No. 34;
5; Mismatches
                                                 EMBL/GenBank/DDBJ databases
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In D., Frise E., George R.,
Miranda A., Mungall C.J.,
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                                                                                                                                                                                                                                                                                                                                                                                    mitochondrial
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                                                                                                                                                                                          Fartmann B.,
                                                                                                                                           databases
                                                                                                                                                                                                                                                                                       Sordariomycetes;
Neurospora.
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Prochnik S.E.,
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Q7SH14
ID Q7SH1
AC Q7SH1
AC Q7SH1
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Jiffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,

RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

RA (Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,

RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,

RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,

RA Kothe G.O., Jedd G., Mewes W., Staben C., Retter A., Schulte U.,

RA ROY A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,

RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,

RA Karystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

ROGONI C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

RA Karystofova S., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

RA Karystofova S., Catcheside D., Li W., Pratt R.J., Osmani S.A.,

RA Varden O., Plamann M., Seiler S., Dunlap J., Voelker R.,

RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,

RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";

RT. "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
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R GO; GO:0006412; P:protein biosynthesis; IEA.
R GO; GO:0006414; P:translational elongation; IEA.
R InterPro; IPR004540; EF-G.
R InterPro; IPR000640; EFG C.
R InterPro; IPR000527; EFG_IU_
R InterPro; IPR000517; EFG_IU_
R InterPro; IPR000517; EFG_IU_
R InterPro; IPR000517; EFG_IU_
R InterPro; IPR000795; ProtSyn GTPbind.
InterPro; IPR000795; ProtSyn GTPbind.
R InterPro; IPR000795; ProtSyn GTPbind.
R InterPro; IPR009000; Translat_factor.
R InterPro; IPR009000; Translat_factor.
R Ffam; PF00679; EFG_C; 1.
R Pfam; PF003764; EFG_IV; 1.
R Pfam; PF003144; GTP_EFTU; 1.
R Pfam; PF03144; GTP_EFTU; 1.
R Pfam; PF03144; GTP_EFTU; 1.
R Pfam; PF03144; GTP_EFTU; 1.
R Pfam; PF0315; ELONGATNECT.
R TIGRFAMS; TIGR00484; EF-G; 1.
R TIGRFAMS; TIGR00481; Small GTP; 1.
R TIGRFAMS; TIGR00481; Small GTP; 1.
R PROSITE; PS00301; EFACTOR_GTP; 1.
R Blongation factor; GTP-binding; Protein biosynthesis.
SEQUENCE 800 AA; 88373 MW; F2A7C425F6D4974A CRC64;
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Best Local :
preliminary data.
EMBL; AABX0100006; EAA36106.1;
HSSP; P13551; 1FNM.
GO; GO:0005577
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
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Q7SH14; PT 813 AA.
Q7SH14; PT 813 AA.
Q1-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Name=NCU02955.1;
                                                                                                                                                    Nature 0:0-0(2003).
-i- CAUTION: The sequence shown
EMBL/GenBank/DDBJ whole geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=OR74A;
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                                                                                                                                                genome
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                                                                                                                                                shotgun
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hotgun (WGS)
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Neurospora.
                                                                                                                                                                                         from an
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AC Q971V
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Best Local (
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Best Local
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InterPro; IPR000795; ProtSyn GTP
InterPro; IPR005225; Small GTP.
InterPro; IPR005225; Small GTP.
InterPro; IPR009000; Translat_fa
Pfam; PP00679; EFG_C; 1.
Pfam; PP003764; EFG_IV; 1.
Pfam; PP00144; GTP_EFTU; 1.
PRINTS; PR00315; ELONGATNECT.
PRINTS; PR00315; ELONGATNECT.
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Q971V5;
01-DEC-2001
01-DEC-2001
01-JUN-2003
                                                                                                                                                                                                            HSSP; P01100; 1FOS.
Complete proteome;
SEQUENCE 311 AA;
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=JCM 10545 / 7;

MEDLINS=21456156; PubMed=11572479;

MEDLINS=21456156; PubMed=11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguch

Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

Oshima T., Kikuchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
Hypothetical protein ST1273.
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TIGREAMS; TIGRO0231; small GTP; 1.
TIGREAMS; TIGRO0231; small GTP; 1.
PROSITE; PS00301; EFACTOR GTP; 1.
GTP-binding; Hypothetical protein; Protein biosynthesis.
SEQUENCE 813 AA; 89810 MW; C9A5093F35B29B05 CRC64;
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InterPro; IPR009022; EFG III V.
InterPro; IPR0052517; EFG IV.
InterPro; IPR0054161; EFTU D2.
InterPro; IPR000795; ProtSyn GTPbind.
InterPro; IPR005225; Small GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfolobus tokodaii.
Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                      Crenarchaeon, Sulfolobus tokodaii
DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=ST1273;
                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=111955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 IKELCEQKRQELIEKLADVDDEIAEMFLEEQTFTPEQIKAAIRRATIACKFTPVLMGSAI 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 A 366
                                                                                                                                                                                                                                                                                            AP000985; BAB66315.1; -.
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71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 28.3%; Score 71; DB 2; Similarity 26.2%; Pred. No. 1e+02; 16; Conservative 14; Mismatches 1
                                                   N
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                                                                                                                                     Similarity
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                                                VKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL
IKQLSQQK-QSLIQVISEIKKEFEQIKNVEK---VKEKLDPLQILKKIEQL 117
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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P:translational elongati
                                                                                                                                                                                                               Hypothetical 37536 MW; 6
                                                                                                                                27.98;
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                                                                                                      Score 70; DB
Pred. No. 50;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
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674338A5E031B429 CRC64;
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                                                                                                            18;
                                                                                                                                                            Length 311;
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Takamiya M., Kacc
Takamiya N., Oguchi A.,
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MEDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
A Adams M.D., Celniker S.E., Holt R.M., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
A Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
A Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
A Ballew R.M., Baseu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
A Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Susam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L., E., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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Best Local
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Q8MQK1;
01-OCT-2002
01-OCT-2002
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01-JUN-2003
01-JUN-2003
01-MAR-2004
CG10971-PB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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ORFNames=CG10971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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GO; GO:0003779; F:actin binding;
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Celniker S.,
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; 85362 MW;
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Pred. No. 1.2e+
9; Mismatches
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Perraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Lin X., Mattel B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lin X., Mattel B., McIntosh T.C., McLeod M.P., Liang Y., Lin X.,
RA McIntoy G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Syler E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang X.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
"The genome sequence of Drosophila melanogaster.";
RT "The genome sequence of Drosophila melanogaster.";
RT Science 287:2185-2195(2000).
   EMBL; AB003540; ARF49884.1; -.
FlyBase; FBgn0036309; CG10971.
GO; GO:0003779; F:actin binding; I
GO; GO:0005543; F:phospholipid bin
InterPro; IPR011417; ANTH.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronm
Patel S., Frise E., Wheeler D.A.,
Patel S. M. Celniker S.E.;
                                                                                                                           SEQUENCE FlyBase;
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Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
                                                                                                                                                                                                                                                                                                                          MEDIINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman H
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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MEDLINE=22426065; PubMed=12537568;
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R.A.,
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DR InterPro; IPR002558; ILWEQ.

DR Pfam; PF07651; ANTH; 1.

DR Pfam; PF07651; ANTH; 1.

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DR Pfam; PF01608; I_LWEQ; 1.

DR PCOLOM; PD011820; ILWEQ; 1.

DR PCOSITE; PS50942; ENTH; 1.

DR PCOSITE; PS50945; I_LWEQ; 1.

SQ SEQUENCE 1087 AA; 124298 MW; C83E709907DFE8E8 CRC64;

Query Match

Best Local Similarity 44.2%; Pred. No. 1.8e+02;

Matches 19; Conservative 9; Mismatches 11; Indels 4; Gaps 2;

Matches 19; CONSERVATIVE 9; Mismatches 11; Indels 4; Gaps 2;

Qy 7 QOKYORLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQL 49

Db 408 KQVNSQLLLETKELTNEISKIKVNVEE---KEK-TNLILQKQI 446

Search completed: November 3, 2005, 22:03:04

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-09-107-532A-587
US-09-269-858A-8
US-09-269-858A-9
US-09-238-092-1321
US-09-248-796A-14974
US-09-081-689-2
US-09-305-984-14
US-09-305-984-16
US-08-487-833-3720
US-08-487-8-33-3720
US-08-478-435-6
US-08-478-373-6
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Sequence 7806, Ap
Sequence 5587, Ap
Sequence 43, Appli
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Sequence 5317, Ap
Sequence 6, Appli
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RESULT 2 Sequence 14 Patent No. GENERAL INF APPLICANT:	Query Ma Best Loo Matches Qy	RESULT 1 US-09-270-76 Sequence 4 Patent No. GENERAL IN APPLICANT ITILE OF FILE REFE CURRENT A CURRENT A CURRENT A CURRENT OF NUMBER OF SOFTMARE: SEQ ID NO SEQ ID NO SEQ ID NO TYPE: PR ORGANISM US-09-270-76		4 4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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40-14908 14908, Applicat . 6833447 . 6833447 . 1872 . REPREMATION: . Slater; Ste T: Goldman, Bar T: Hinkle, Gre T: Wiegand, Ro INVENTION: Myx ERENCE: 38-10(14 APPLICATION NUM FILING DATE: 2 FILICATION NUM FILING DATE: 2000 FILION DATE: 2000 FILIO	Conser Conser CETPQQK	57-43370 Applica 6703491 FORMATION: F: Homburger e INVENTION: File File File File File GATE: FILING DATE: FILING DATE: FILE JACON IN FILING DATE:		23.5 23.5 23.5 23.5 23.5 23.5 23.5 23.5
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ces and Uses Thereof	Length 142; ; Indels 0; Gaps 0;	Drosophila melanogaster		Sequence 13, Appl Sequence 12, Appl Sequence 18800, A Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7646, Ap Sequence 7646, Ap Sequence 7646, Ap Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 6466, Ap Sequence 8325, Ap

Query Match

25.7%;

Score 64.5;

DB

Length 639;

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RESULT 4
US-09-107-532A-5587
J Sequence 5587, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
ITILE OF INVENTION: NUCLEIC ACID
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APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
PILE REFERENCE: 59 US2.REG
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SEQ ID NO 7806
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: PC
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
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                                                                                                             STATE: Massachusetts
                                                                                                                                CITY: Waltham
OPERATING SYSTEM: <Unknown>
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Matches 15; Conserv
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Query Match 25.1%; Score 63; DB Best Local Similarity 30.9%; Pred. No. 28; Matches 17; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Angerer, Bernhard
APPLICANT: Ankenbauer, Waltraud
APPLICANT: Boehringer, M.
APPLICANT: Bonch-Osmolovskaya, Elizaveta
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/269,858A CURRENT FILING DATE: 1999-06-10 PRIOR APPLICATION NUMBER: PCT/EP97/05390 PRIOR FILING DATE: 1996-10-03
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Markau, Ursula
APPLICANT: Reiser, Astrid
APPLICANT: Schmitz-Agheguian, Gudrun
APPLICANT: Svetlichny, Vitaly
TITLE OF INVENTION: Thermostable DNA Polymerase
FILE REFERENCE: 4452
                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: EP/96115877 PRIOR FILING DATE: 1996-10-03
                                                                                                                            LENGTH: 85
TYPE: PRT
                                                                                                        ORGANISM: Abedus herberti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 5587: SEQUENCE CHARACTERISTICS: LENGTH: 193 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATE: APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEE 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                1996-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.5%;
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                                           DB 4; Length 850;
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    Indels
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GVKETPQQKYQRLLHE----VQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52

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RESULT 8
US-09-248-796A-14974
; Sequence 14974, Application US/09248796A
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                                                                                                                                                                                                                                                                                           ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14203
US-09-538-092-1321
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US-09-623-326-43
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TITLE OF INVENTION: Polymerase Chimerase;
FILE REFERENCE: 4894
CURRENT APPLICATION NUMBER: US/09/623,326;
CURRENT FILING DATE: 2001-02-08;
PRIOR APPLICATION NUMBER: DE 198 10 879.6;
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                              Query Match 24.9%; Score 62.5; I
Best Local Similarity 34.8%; Pred. No. 52;
Matches 16; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1321
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LENGTH: 851
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Anaerocellum thermophilum -09-623-326-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
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APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILB REFERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: CuraPatSeqFormatter Version 0.9
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                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                          ETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQL 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVKGIGEKSAOKLLEEYSSLEEIYONLDKIKSSIREKLEAGK-DMAFLSKRLATI 245
                                                                                                                                 ESLQQEVEALKERVDELTTDLEILKAEIEEKGSDGAASSYQL-KQL 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 851
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PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14974
LENGTH: 309
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-14974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-081-689-2
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Best Local Similarity 41.2
14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6165992
                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 442 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Wallis, Nicola G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN: TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE.REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                         REFERENCE/DOCKET NUMBER: GM.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 30-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Biswas, Sanjoy
TITLE OF INVENTION: Histidine Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                   STRANDEDNESS:
                                                                                                                         TELEPHONE:
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CITY: Philadelphia
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                amino acid
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                                                                                                                           215-994-2222
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linear
               single
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Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33
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PATENT NO. 6331407

GENERAL INFORMATION:
APPLICANT: No. 6331407ak, Rodger
APPLICANT: TOUMANDEN, Elaine
ITILE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF
FILE REFERENCE: 1340-1-016N1
CURRENT APPLICATION NUMBER: US/09/305,984B
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: 60/084,399
EARLIER APPLICATION NUMBER: 09/305,984
RESULT 12
US-09-493-940-14
; Sequence 14, A
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US-09-305-984-14
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                                                                                                                                                                                                                                                                                                                                SOFTWARE: 1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6448224
GENERAL INFORMATION:
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Best Local S
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                APPLICANT: No. 6448224ak, Rodger
APPLICANT: Toumanen, Elaine
TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
FILE REFERENCE: 1340-1-016
CURRENT APPLICATION NUMBER: US/09/073,541A
CURRENT FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                      LENGTH: 442
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 442
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                                                                                                                                                                            18; Conservative
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                                                                                                Application US/09305984B
    Application US/09493940
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                                                                                                                                                                          ; Score 61; DB ; Pred. No. 23; 6; Mismatches
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; Pred. No. 23;
6; Mismatches
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                                                                                                                                                                                              DB 4; Length 442; 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 442; 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Length 442
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FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR PILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 5317
LENGTH: 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Streptococcus pneumoniae US-09-493-940-14
                                                                                                                                                                                                                                                            밁
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US-09-583-110-5317
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                                                                                                                                                                             RESULT 14
US-09-107-433-3720
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-583-110-5317
          Patent No. 6630583
GENERAL INFORMATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5317, App
Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 24.3%;
Best Local Similarity 33.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/493,940
CURRENT FILLING DATE: 2000-01-28
EARLIER APPLICATION NUMBER: 60/084,399
EARLIER FILING DATE: 1998-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JENERAL INFORMATION:
APPLICANT: No. 6630583ak, Rodger
APPLICANT: Toumanen, Blaine
TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS
FILE REFERENCE: 1340-1-016N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 09/305,984
EARLIER FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                             Local Similarity
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 LKEQINSLYOHLLTVIADLHEKNEAILQLEKMKVEFLRGASHELKTPLASLKIL 253
                                                                                                                                                                                                                                                            200 LKEQINSLYOHLLTVIADLHEKNEAILQLEKMKVEFLRGASHELKTPLASLKIL 253
                                                                                                                                                                                                                                                                                                                                          18;
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                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                           24.3%;
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Pred. No. 23;
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Pred. No. 23;
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                                                           FOR DIAGNOS
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CITY: Waltham

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

100 Beaver Street

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NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...446;
SEQUENCE DESCRIPTION: SEQ ID NO: 3720:
US-09-107-433-3720
                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-08-487-890A-6
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Best Local Similarity 33.3%;
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Patent No. 5708149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3720: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                            APPLICANT:
TITLE OF IN
                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                 APPLICANT:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                    APPLICANT:
                                                               STREET: 6th F1
                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489 REFERENCE/DOCKET NUMBER: GTC-011 TELECOMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNAY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/107,433 FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 LKEQINSLYQHLLTVIADLHEKNEAILQLEKMKVEFLRGASHELKTPLASLKIL 257
                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VKETPQQKYQRL-----LHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
                                                                                                                                                            INVENTION:
                               Ontario
(: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (781)893-500
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 446 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                      6th Floor, 330 Unviersity Avenue
                                                                                                                                                    Chong, Pele
Gray-Owen, Scott
Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
VENTION: Transferrin Receptor Genes
                                                                                                                                                                                                                                                                 Schryvers, Anthony
                                                                                                                                                                                                                                                                                      Loosmore, Sheena
Harkness, Robin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02354
                                                                                                                                           147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61; DB 4; Length 446; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FACE BIOSK (F2010)
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Query Match 24.3%; Best Local Similarity 32.6%; Matches 15; Conservative
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                                                                                                                                             ; TOPOLOGY: US-08-487-890A-6
                                                                                                                                                                                                                                                       TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
                                                                                                                                                                                                                                                                                                      NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 08-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                TELEPHONE: (416) E
                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
244 LRETDANKSONRTHKLYDLEADVHSNRFRGKVKPTKKESSEEHPFT 289
                                   2 VKETPQQKYQRLLHEVQELTTEVE-----KIKTTVKESATEEKLT 41
                                                                                                                                                                                              amino acids
                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                          (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/148,968
                                                                     ; Score 61; DB:
; Pred. No. 36;
8; Mismatches
                                                                                                       DB 1; Length 644;
                                                                       17;
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                                                                       6,
                                                                   Gaps
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Search completed: November 3, 2005, 22:05:57
Job time : 27.6952 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
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251
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*

1: /cgn2_6/ptodate/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodate/1/pubpaa/PCT_NEW_PUB.pep:*

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6: /cgn2_6/ptodate/1/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/I/pubpaa/USO9E_PUBCOMB_pep:*
/cgn2_6/ptodata/I/pubpaa/USO9E_PUBCOMB_pep:*
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/cgn2_6/ptodata/I/pubpaa/USO9E_PUBCOMB_pep:*
/cgn2_6/ptodata/I/pubpaa/USO9E_PUBCOMB_pep:*
/cgn2_6/ptodata/I/pubpaa/USOP_PUBCOMB_pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11	10	9	8	7	σ	ທ	4	w	2		No.
103	107	113	231	246	248	248	251	251	251	251	Score
41.0	42.6	45.0	92.0	98.0	98.8	98.8	100.0	100.0	100.0	100.0	Query Match Length DB
20	21	22	134	52	224	183	465	465	406	401	ength
10	10	10	14	10	16	10	14	9	10	16	: B
US-09-782-816A-5	US-09-782-816A-4	US-09-782-816A-3	US-10-106-698-6730	US-09-782-816A-51	US-10-425-115-315831	US-09-782-816A-54	US-10-102-806-676	US-09-925-298-676	US-09-782-816A-53	US-10-408-765A-1369	ID
Sequence 5, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 6730, Ap	Sequence 51, Appl	Sequence 315831,	Sequence 54, Appl	Sequence 676, App	Sequence 676, App	Sequence 53, Appl	Sequence 1369, Ap	Description

4 5	44	43	42	41	40	39	38	37	36	35	3 <u>4</u>	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	1
64	64	64	64	64	64	64	64	64	4	65.5	'n	66	66	67	67	67	67	68	68	70	70	70.5	70.5	71	72.5	72.5	1	76	81	88	93	98	100
25.5		•		•	•	25.5	•	•	•	•	•	•		26.7	•	•	26.7	•	27.1	27.9	27.9	28.1	28.1	•	•	•	•	•		35.1	٠	٠	٠
188	188	188	188	188	188	188	188	185	348	1837	576	386	13	2481	2478	2478	2478	2368	2368	1087	1087	356	348	14	380	œ	53	15	16	17	18	19	,
14	14	14	14	14	14	14	10	16	16	15	15	15	10	15	17	9				20	20	15	16	10	20	10	10	10	10	10	10	10	
0 - 17	5-746-	0-140-47	US-10-123-904-2	0-121-049-	-10-140-808-	-072-	9-284-320-	-740-	US-10-437-963-139713	-10-369-	US-10-424-599-274041	-10	ū	US-10-282-122A-43762	US-10-470-048B-220	US-09-815-242-12967	9-815-242-	-242-	-242-563	-11-097-143	-11-097-143-	-10	-10-425-115	-09-782-	-11-097-143-4	-816A-	-09-782-	-09-782-816A-	-09-782-816A-	-09-782-	-09-782-816A-	-09-782-816A-	07 100 01011
Ф 22	e 2,	e 2,	e 2,	æ	e 2,	e 2,	e 12	Θ ω,	O	Sequence 22734, A	e 27404	e 71967,	e 12, /	æ	ce 220,	_	5816,	1238	5635,	(D N)	0		.,	e 11	e 40	e 56	e 52	e 10	e 9,	Sequence 8, Appli	e 7,	е 6,	+

ALIGNMENTS

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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faby, Eoin D.
APPLICANT: Jang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Glemn, Gary M.
APPLICANT: Taylor, Steven W.
APPLICANT: Glemn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOM
FILE REFERENCE: 660088 465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILLING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1369
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                                                                                                                                                                                                    ; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-408-765A-1369
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                                                                                                  Query Match 100.0%; Score 251; DB 16; Best Local Similarity 100.0%; Pred. No. 1.5e-19; Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1369, Application US/10408765A
Publication No. US20040101874A1
  94 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 145
                                   1 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
                                                                                                                                                Length 401;
                                                                                                       Indels
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                                                                                                     0;
                                                                                                     Gaps
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0;

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PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR PRICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 676
В
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                                                                                                                                                   NAME/KEY: SITE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring US-09-925-298-676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-925-298-676
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APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 676, Application US/09925298 Publication No. US20020039764A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 53
                                                                           Matches
                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
                                                                                                                                                                                                                                                                              NAME/KEY: SITE LOCATION: (5)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 406
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                          NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                FEATURE:
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158 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 150
                                                                         52;
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                     1 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
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                                                                         Conservative
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                                                                       100.0%; Score 251; DB 9;
100.0%; Pred. No. 1.8e-19;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                            naturally
                                                                                                             Length 465;
                                                                       Indels
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RESULT 4 US-10-102-806-676

RESULT 6 US-10-425-115-315831

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CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
FRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: F07/S00/05881
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 676
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                                                                                                                                                                        ; TYPE: PRT ; ORGANISM: Mus musculus US-09-782-816A-54
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US-09-782-816A-54
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                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 183
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Sharp, David J.

APPLICANT: Rogers, Gregory C.

APPLICANT: Scholey, Jonathon M.

TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR

TITLE OF INVENTION: PROLIFERATION

FILE REFERENCE: UC069.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 54, Application US/09782816A Publication No. US20030032771A1
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                                                                                    Query Match 98.8%;
Best Local Similarity 98.1%;
Matches 51; Conservative
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAMES/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 465
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE LOCATION: (16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 100.0%;
Local Similarity 100.0%;
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  94
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                           1 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVVLAKQLAAL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/10102806 o. US20030054421A1
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                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                         Score 248; DB 10;
Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 251; DB 14;
Pred. No. 1.8e-19;
                                                                                      Mismatches
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                                                                                      0;
                                                                                                                               Length 183;
                                                                                    Indels
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                                                                                    Gaps
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RESULT 8
US-10-106-698-6730
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APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CEITILE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
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US-10-425-115-315831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 56

SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 51

LENGTH: 52

TYPE: PRT

ORGANISM: Unknown
          GENERAL INFORMATION:
APPLICANT: Ruben et
TITLE OF INVENTION:
                                                                   Sequence 6730, Application US/10106698 Publication No. US20030109690A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51, Application US/09782816A Publication No. US20030032771A1
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SEQ ID NO 315831
LENGTH: 224
                                                                                                                                                                                                                                                                                               Best
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleaic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                        09-782-816A-51
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CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic, David
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: UNSURE
LOCATION: 44
OTHER INFORMATION: Xaa = Val or Leu
OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
OTHER INFORMATION: musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                   1 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
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                                                                                                                                                                                                                                                                      h 98.0%;
Similarity 98.1%;
51; Conservative
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Kovalic, David K.
al.
Colon and Colon Cancer Associated Polynucleotides and Polypeptide
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98.1%;
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Pred. No. 5e-20;
0; Mismatches
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Pred. No. 1.7e-19;
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                                                                                                                                                                                                                                                                                                              DB 10;
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                                                                                                                                                                                                                                                                                                              Length 52;
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RESULT 10
US-09-782-816A-4
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                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 22
TYPES TO STATE OF THE SECOND SECON
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PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 6730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09782816A Publication No. US20030032771A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR, APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: A sequence conserved OTHER INFORMATION: musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC FEATURE LOCATION: (126)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
                                                                                                                                                                                                  GVKETPQQKYQRLLHEVQELTT 22
                                                                                                                                                          GVKETPQQKYQRLLHEVQELTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                         45.0%;
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                                                                                                                                                                                                                                                                                                                                         Score 113; DB 10;
Pred. No. 1.1e-05;
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Pred. No. 7.1e-18;
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                                                                                                                                                                                                                                                                                                                                                                                 Length 22;
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Sequence 4, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION

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Sequence 5, Application US/09782816A
PUBLICATION NO. US20030032771A1
GENERAL IMFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Roders, Jonathon M.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT APPLICATION DATE: 2001-02-14
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                            APPLICANT: Sharp, David J.

APPLICANT: ROGETS, Gregory C.

APPLICANT: Scholey, Jonathon M.

ATITLE OF INVENTION: PEPTIDE INHIBITORS OF CEI

TITLE OF INVENTION: PROLIFERATION

FILE REFERENCE: UC069.001A

CURRENT APPLICATION NUMBER: US/09/782,816A

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 21
TYPE: PRT
ORGANISM: Unknown
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
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Best Local (
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               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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-09-782-816A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: UC069.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus OTHER INFORMATION: musculus.
LENGTH: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 100.
20; Conservative
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100.0%; Pre
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100.0%;
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%; Pred. No. 0.0
0; Mismatches
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                                                                                                                                               OF CELLULAR
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hes 0;
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Sequence 6, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CEL
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069 001A
FILE REFERENCE: UC069 001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                 APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Rogers, Gregory C.
APPLICANT: Rogers, Gregory C.
ITITLE OF INVENTION: PEPTIDE INHIBITORS OF CEI
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CEI
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus; OTHER INFORMATION: musculus. US-09-782-816A-6
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US-09-782-816A-7
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US-09-782-816A-6
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                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09782816A Publication No. US20030032771A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local :
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ORGANISM: Unknown
FEATURE:
NAME/KEY: UNSURE
LOCATION: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Unknown FEATURE:
           TYPE: PRT
ORGANISM: Unknown
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FEATURE:
                                                     ENGTH: 18
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Pred. No. 0.
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d a Mus musculus sequence when
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0.00042;
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APPLICANT: Sharp, David J.

APPLICANT: Rogers, Gregory C.

APPLICANT: Rogers, Gregory C.

APPLICANT: Rochery, Jonathon M.

TITLE OF INVENTION: PEDTIDE INHIBITORS OF CELLULAR

TITLE OF INVENTION: PROLIFERATION

FILE REFERENCE: UC069.001A

CURRENT APPLICATION UNMEER: US/09/782,816A

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENCTH: 17

TYPE: PRT

ORGANISM: Unknown

FEATURE:

FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus; OTHER INFORMATION: musculus. US-09-782-816A-7
Search completed: November 3, 2005, 22:11:40 Job time: 93.7112 secs
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                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus; OTHER INFORMATION: musculus.
US-09-782-816A-8
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                                                                                                                                                                                  Query Match 35.1%; Score 88; DB 10; Length 17; Best Local Similarity 100.0%; Pred. No. 0.0048; Matches 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.1%; Score 93; DB 10; Length 18; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 18; Conservative 0; Mismatches 0; Indels
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SUMMARIES

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ADD47033	ADD47861	ADD47857	ADD47855	ADD47859	ADB79862	AAM77711	ABB26895	ABG41658	ABG53529	AAM59298	AAM71845	ABB23745	AAM32130	ABB38669	AAM19334	ABP53000	ABG41126	ABG53031	AAM58807
Add47033	Add47861	Add47857	Add47855	Add47859	Adb79862	Aam77711	Abb26895	Abg41658	Abg53529	Aam59298	Aam71845	Abb23745	Aam32130	Abb38669	Aam19334	Abp53000	Abg41126	Abg53031	Aam58807
Human Pro	Human Pro	Human Pro	Rat Prote	Rat Prote	Rat myosi	Human bon	Protein #	Human pep	Human liv	Human bra	Human bon			Peptide #	Peptide #	Cellular	Human pep	Human liv	Human bra

ALIGNMENTS

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RESULT 1
ABP53017
ID ABP5
p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                   ABP53017;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP53017 standard; peptide;
                                                                                                                                                                                                                                           22-AUG-2002.
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                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                           Cellular proliferation inhibition; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                             Cellular proliferation peptide inhibitor SEQ ID NO:52.
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                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; cancer;
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21-JAN-2002; 2002WO-US001708.

14-FEB-2001; 2001US-00782816.

(REGC) UNIV CALIFORNIA.

Sharp DJ, Rogers GC, Scholey JM;

WPI; 2002-657599/70.

New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders. λĀ

Claim 3; Page 31; 55pp; English.

The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such

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Best Local Similarity
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                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000;
11-JUL-2000;
                                                                                                 Sequence 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
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98.1%;
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   Score 243.5; DB 4
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Pred. No. 2.4e-26;
; Mismatches 0;
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GEKETPVQKCQRLQIEMNELLNEVAALQVDRKVADEEKQSYDAVVATVISTAR 53

Matches Query Match Best Local

Similarity

94.4%;

Score 243.5; DB 5 Pred. No. 2.4e-23;

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Indels Length 380;

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                                                                                                                                                       The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomaes, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastcocelic disorders. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocelic disorder; angiogenic disorder; immunologic disorder; p50.
                                                         inflammatory, angiogenic and immunologic disorders. The present sequence represents Drosophila melanogaster p50 which is given in the exemplification of the present invention
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
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22-AUG-2002

21-JAN-2002; 2002WO-US001708

14-FEB-2001; 2001US-00782816

(REGC) UNIV CALIFORNIA.

ე. მ Scholey JM;

WPI; 2002-657599/70

New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors; leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

Claim 1; Page 30; 55pp; English

The present invention describes an isolated peptide (I) comprising or CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-CC terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The CC peptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibitors cellular proliferation, such CC as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and ceck tumours); leukaemias and lymphoid malignancies, other disorders such CC as neuronal, glial, astrocytal, hypothalamic and other glandular, CC macrophagal, epithelial, stromal and blastocoelic disorders; and CC inflammatory, angiogenic and immunologic disorders. The present sequence cropresents a peptide that can be N-terminally added to (P2)

Sequence 22 AA;

Matches Query Match Best Local 22; Similarity Conservative 44.2%; 100.0%; 0; Score 114; Pred. No. Mismatches 8e-08 명 υ --0, Length 22 Indels 0, Gaps

22

밁 S GEKETPVOKCORLQIEMNELLN 22

> Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder; ABP52992 WPI; 2002-657599/70 Sharp DJ, 14-FEB-2001; 2001US-00782816 21-JAN-2002; 2002WO-US001708 22-AUG-2002 Drosophila melanogaster Cellular proliferation inhibitor related peptide SEQ ID NO:27 05-NOV-2002 ABP52992 standard; peptide; 21 AA immunologic disorder. Rogers GC, (first entry) Scholey JM;

New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.

Claim 1; Page 30; 55pp; English.

The present invention describes an isolated peptide (I) comprising or CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-CC terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The CC peptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such CC as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and CC neck tumours); leukaemias and lymphoid malignancies, other disorders such CC macrophagal, spithelial, stroogtal, hypothalamic and other glandular, CC inflammatory, angiogenic and immunologic disorders. The present sequence crepresents a peptide that can be N-terminally added to (P2)

Sequence 21 A A

Matches Query Match Best Local 21; N Similarity EKETPVOKCORLOIEMNELLN 22 41.9%; ilarity 100.0%; Conservative 0, Score 108; Pred. No. Mismatches 4.7e-07; DB 5 0 Length 21; Indels ٥, Gaps

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RESULT 6
ABP52967
ID ABP5

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EKETPVQKCQRLQIEMNELLN

21

ABP52967 standard; peptide; 22 A

ABP52967;

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RESULT 7
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   Cellular proliferation inhibition; cytostatic; antiinflammatory; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcino
                                                                                            Cellular proliferation inhibitor related peptide SEQ ID NO:28
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ilarity 100.0%;
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Pred. No. 1.
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CC The present invention describes an isolated peptide (I) comprising or CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-CC terminal extensions. (I) have cytostatic and antinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The CC peptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such CC as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC thyroid, hepatic carcinomas, sarcomas, glioblatcomas, and various head and CC as neuronal, glial, astrocytal, hypothalamic and other glandular, CC macrophagal, epithelial, stromal and blastcocelic disorders; and CC inflammatory, angiogenic and immunologic disorders. The present sequence CC represents a peptide that can be N-terminally added to (P2)
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                                                                                                                                                                                                                                                                                                                                                                                                 New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
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Best Loc Matches Query Match Local w 20; Similarity KETPVQKCQRLQIEMNELLN Conservative 39.9%; 0 Score 103; Pred. No. 22 Mismatches DB 5; 2e-06; 0 Length 20 Indels 0, Gaps 0

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KETPVOKCORLOIEMNELLN

20

ABP52994 standard; peptide; 19

05-NOV-2002 (first entry)

Cellular proliferation inhibitor related peptide SEQ ü NO:29.

RESULT 8
ABP5294
ID ABP5
XX ABP5
XX ABP5
XX C05-N
XX C011
XX C sarcoma, glioblatoma; leukaemia; lymphoid malignancy; carcinoma; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; gliandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder: immunologic disorder

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ABP52995
ID ABP7
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                                                                                                                                                                                    Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
                                  WO200264779-A2
                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                     Cellular proliferation inhibitor related peptide SEQ ID NO:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP52995
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Pred. No.
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ABP52996
ID ABP5
RESULT 10
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Matches
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                                                                                                                                                                     Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; pso inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; satrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
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                                                                                                                           Drosophila melanogaster.
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14-FEB-2001; 2001US-00782816

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ABP52997
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Best Local 9
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                                    Sharp DJ,
                                                                                                   (REGC ) UNIV CALIFORNIA
                                                                                                                                                               14-FEB-2001;
                                                                                                                                                                                                                              21-JAN-2002; 2002WO-US001708
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stromal disorder; blastocoelic disorder; angiogenic disorder;
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                                    Scholey JM
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Claim 1; Page 30; 55pp; English
                                                                                                                                                                                   New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
                                                                                                                                                                          immunologic disorders.
                                                                                                                                                                                                                       WPI; 2002-657599/70
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The present invention describes an isolated peptide (I) comprising or CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-CC terminal extensions. (I) have cytostatic and antiinflammatory activities CC and can be used as p50/dynamitin inhibitors and in gene therapy. The CC peptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such CC as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and CC neck tumours); leukaemias and lymphoid malignancies, other disorders such CC as neuronal, glial, astrocytal, hypothalamic and other glandular, CC macrophagal, epithelial, stromal and blastocoelic disorders; and CC represents a peptide that can be N-terminally added to (P2)

16 AA;

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              á
                                  Matches
                                          Query Match
Best Local Similarity
                                  16;
1 VOKCORLOIEMNELLN 16
           7 VQKCQRLQIEMNELLN 22
                                 Conservative
                                          31.4%; Score 81; 100.0%; Pred. No.
                                  0
                                   Mismatches
                                          DB 5;
0.0012;
                                    0
                                                  Length 16;
                                   Indels
                                  0;
                                  Gaps
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0

Cellular proliferation inhibitor related peptide SEQ ID NO:33. 05-NOV-2002 ABP52998 standard; peptide; 15 (first entry)

p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder; Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; immunologic disorder.

Drosophila melanogaster

WO200264779-A2

21-JAN-2002; 2002WO-US001708

14-FEB-2001; 2001US-00782816

(REGC) UNIV CALIFORNIA

짇 Rogers GC, Scholey JM

WPI; 2002-657599/70.

New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and

Claim 1; Page 30; 55pp; English.

immunologic disorders

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RESULT 13
ABP53019
ID ABP53
XX Collaps
XX Collaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
                                                                                                                   New peptide inhibitors of p50/dynamitin useful for tinhibiting cellular proliferation, e.g. benign or maleukemia and lymphoid malignancies, or inflammatory, immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2001; 2001US-00782816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2002; 2002WO-US001708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cellular proliferation inhibition; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP53019 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200264779-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse p50 amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunologic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OKCORLOIEMNELLN
                                                                                                                                                                                                                                                                                                                                           Rogers GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.8%; Score 77; ilarity 100.0%; Pred. No. Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā,
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                                                                                                                                                                                                                                                                                                                                              Scholey JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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0.0038;
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                                                                                                                                                                                      for treating cancer by or malignant tumors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory;
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Disclosure;

Fig 2; 55pp; English

The present invention describes an

isolated peptide (I) comprising

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RESULT 14
ABP53
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ABP53
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ABP53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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                            New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cellular proliferation peptide inhibitor SEQ ID NO:51.
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                                                                                                                                                                                                                                                                                                                                                         14-FEB-2001; 2001US-00782816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP53016 standard;
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                                                                                                                                                                                                                                      Sharp DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2002; 2002WO-US001708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glandular disorder; macrophagal disorder; stromal disorder; blastocoelic disorder;
                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunologic
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19; Conser
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                                                                                                                                                                                                                                      Rogers GC,
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                                                                                                                                                                                                                                         Scholey JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       angiogenic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorder;
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Claim 2; Page 31; 55pp; English.

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RESULT 15
ABM81421
ID ABM81421
XX ABM81
AC ABM81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                     New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ:3675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                 Wu TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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The invention relates to human tumour-associated antigenic target (TAT)

Claim 12; SEQ ID NO 3675; 7273pp; English

prostate cancer or tumor.

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                                                 CC polypeptides, and their related nucleic acids. The TAT polypeptides are CC overexpressed in cancer tissues compared to normal tissues, and may thus CC serve as effective targets for the diagnosis and treatment of cancer in CC mammals. The invention also relates to nucleic acid and polypeptide CC polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic CC molecule which binds to a TAT polypeptide; a peptide or organic CC molecule which binds to a TAT polypeptide; apptide or organic CC molecule which binds and compositions for the treatment or CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, CC antibodies, antagonists, binding molecules and compositions are useful CC for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central CC cancer, pancreatic cancer, cervical cancer, cancers of the central CC cancer, melanoma and leukaemia. TAT nucleic acids may further be CC used as hybridisation probes, in chromosome and gene mapping, in CC chromosome identification and in gene therapy. The present sequence
Sequence 314 AA;
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밁 Ś J GEKETPVOKCORLQIEMNELLNEVAALQVD-RKVADEEK 38 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEK 45

1

Query Match Best Local S Matches 19

Similarity

28.1%; 48.7%;

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Score 72.5; DB 8; Length 314; Pred. No. 0.71; Indels

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Search completed: November Job time: 73.5562 secs ω ' 2005, 21:57:31

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57.5	57.5	57.5	57.5	57.5	57.5	57.5	58	58	58	58	58	58	58	58	58
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876	791	629	560	410	272	271	2297	1255	872	866	650	621	463	412	223
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myosin heavy chain	hypothetical prote	hypothetical prote	protein YKR029c ho	hypothetical prote	giardin beta chain	33K cytoskeletal p	hypothetical prote	diaphanous protein	hypothetical prote	paramyosin - Caeno	endostyle-specific	myosin heavy chain	argininosuccinate	myosin heavy chain	hemagglutinin HA2

ALIGNMENTS

RESULT 138055

-	138055
_	myosin heavy chain, perinatai skeletai muscle - human N.Contains: myosin ATPAse (RC 3 6.4 1)
	C; Species: Homo sapiens (man)
-	C;Date: 17-May-1996 #sequence revision 17-May-1996 #text_change 09-Jul-2004
	R; Tullian, E.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman, R.; Schiaffino, S.; Stedman, H.H.
	Eur. J. Biochem. 230, 1001-1006, 1995
	A;Title: Characterization of a human perinatal myosin heavy-chain transcript. A:Reference number: I38055; MUID:95324556; PMID:7601129
	A; Accession: 138055
	A;Status: preliminary; translated from GB/EMBL/DDBJ
	A,Residues: 1-1937 <res></res>
nted,	A;Cross-references: UNIPROT:P13535; EMBL:Z38133; NID:q558668; PIDN:CAA86293.1; PID:q5586
_	R;Karsch-Mizrachi, I.; Feghali, R.; Shows, T.B.; Leinwand, L.A.
	Gene 89, 289-294, 1990
	A, Title: Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA.
	A)RELECETICE IMMOET: UNULUTY MULUTYUSZSSSI; EMIDTZSSSI:
	A; Molecule type: mRNA
	A;Residues: 1-14,'A',16-859 <kar></kar>
y chain	A;Cross-reterences: GB:Y00821
1 proce	A, Experimental source: skeletal muscle
1 prote	submitted to the EMBI, Data Library, January 1989
l prote	A; Reference number: S12458
1 prote	A;Accession: S12459
ypothet	A; Molecule type: mRNA
y chain	A,Residues: 502-1071,'N',1073-1250,'DGG',1253-1376,'NT',1379-1913,'D',1915-1937 <bob></bob>
y chain	A;Cross-releances: EmbL:X51592; NLD:g29465; FIDN:CAA35941.1; FID:g29466
) prote	R:Bober E.: Buchberger-Seidl. A.: Braun T.: Singh. S.: Goedde H.W.: Arnold. H.H.
um upta	Eur. J. Biochem. 189, 55-65, 1990
y chain	A; Title: Identification of three developmentally controlled isoforms of human myosin hea
osin he	A;Reference number: 809331; MUID:90235862; PMID:1691980
ypothet	A; Molecule type: mana
secre	A;Residues: 502-547,'X',549-617,'X',619-687,'X',689-757,'X',759-827,'X',829-897,'X',899-
l prote	-1376,'NT',1379-1386,'X',1388-1456,'X',1458-1526,'X',1528-1596,'X',1598-1666,'X',1668-17
l prote	A; Cross-references: EMBL: X51592
1 prote	J. Cell Biol. 108. 1791-1797. 1989
rter -	A; Title: Molecular genetic characterization of a developmentally regulated human perinat
y chain	A; Reference number: A30220; MUID:89234168; PMID:2715179
y chain	A;ACCESSION: A3UZZU
l prote	A:Molecule type: mRNA
erate m	A, Residues: 860-969, 'Q', 971-1246, 'H', 1248-1260, 'G', 1262-1296, 'Q', 1298-1503, 'AH', 1506-184
on subs	A;Cross-references: GB:Y00821; NID:g34863; PIDN:CAA68757.1; PID:g34864
y chain	C; Genetics:

myosin heavy

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C;Keywords: actin binding; ATP; coiled coil; hydrolase; muscle (F;91-769/Domain: myosin motor domain homology F;181-188/Region: nucleotide-binding motif A (P-loop) F;551-588/Region: actin binding #status predicted F;658-680/Region: Sz #status predicted F;698,708/Active site.
                        A; Molecule type: DNA
A; Residues: 1-297 < KAW>
                                                                                           DNA Res. 6, 83-101, 1999
A;TItle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72670
                                                                                                                                                                                                                                      hypothetical protein APE0790 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H72670
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M. ok, C.; Schlueter, T.; Sensmes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AC1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC1523
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C;Species: Listeria innocua
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C; Superfamily: myosin heavy chain;
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A; Cross-references:
A;Cross-references: UNIPROT:Q9YDX9; DDBJ:AP000060; NID:g5104188; PIDN:BAA79768.1; PID:dl
                                                                                                                                                                                       R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q92DT9; GB:AL592022; PIDN:CAC95955.1; PID:g16413175; GSPDB:
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-230 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Glaser, P.; Frangeul, L.; .; Dominguez-Bernal, G.; Duc
                                                                       A;Status: preliminary
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22; Conserv
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larity 28.9%; Pred. No. 12;
Conservative 15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.9%; Score 69.5; I
30.5%; Pred. No. 1.6;
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; chaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; l
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Fsihi, H.
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RESULT 6

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5 TPVQKCQRLQIEMNELLNEVAALQVDRKVADEEKQSYD 42

SPVREVPNSLLPLNEILNEYIRLKKEKIVMDQEKSKLD

Matches

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Conservative

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Indels

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A;Experimental source:
C;Genetics:
A;Gene: APE0790
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(R8479)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84799
                                                                                                                                                                                                                                     A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                             R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
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A;Cross-references: UNIPROT:066547;
A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; nucleic acid sequence not shown; translation not A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein aq 157 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-
C;Accession: H70314
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A; Residues: 1-508 < STO>
                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                  A; Reference number: A84420; A; Accession: C84799
                                                                                                                                                                                                                                                                              Nature 402, 761-768,
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18; Conservative
                    Similarity
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Score 66; DB Pred. No. 9.1; 10; Mismatches
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Pred. No. 1.9;
13; Mismatches
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Pred. No. 3.1;
                                                                                                                                        GB:AE002093; NID:g4895188; PIDN:AAD32775.1; GSPDB:GN
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myosin heavy chain, fast skeletal muscle - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00084; S14807
R;Maeda, K.; Sczakiel, G.; Wittinghofer, A.
Bur. J. Blochem. 167, 97-102, 1987
A;Title: Characterization of cDNA coding for the complete light meromyosin A;Reference number: S00084; MUID:87304245; PMID:3305014
A;Mccession: S00084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodgon, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber, Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935
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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
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A;Accession: T38346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein SPAC24C9.05c - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9PK98; GB:AE002325; GB:AE002160; NID:g7190604; PIDN:AAF394(
A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-157 < TET>
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A; Residues: 1-730 < MUR>
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Accession: B81688
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                           EKTAPVSDCKKLEAELKQFLKEVAVAK-DRYLQRWRENVYRSLPGVHAIVKKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDAVVATVIST 51
                                                                                                                                                                                                                                                                                                                                                                       EKETPVOKCORLOIEMNELLNEVAALQVDRKVADEEKOSYDAV--VATVISTAR 53
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ce: strain 972h-; cosmid c24C9
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28.2%;
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; Pred. No. 17;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64.5; DI
Pred. No. 3.9;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fission yeast (Schizosaccharomyces pombe)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 157;
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Salzberg,
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A;Residues: 1-698 <GAL)
A;Cross-references: UNIPROT:Q91208; EMBL:Z48794; NID:g755770; PIDN:CAA88724.1; PID:g7557
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP
                                                                                                                                                                                                                                                                                                                                                                                                              myosin heavy chain, fast skeletal muscle, adult [validated] - chicken N;Contains: myosin ATPase (EC 3.6.4.1) C;Species: Gallus gallus (chicken) C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 09-Jul-2004 C;Date: 9x0051; Px0051; Px0052; Dx0051; Px0053; Px
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: Service R;Gauvry, L.1; Fauconneau, B.B. submitted to the EMBL Data Library, March submitted to the EMBL of a fast skeletal
A;Cross-references: UNIPROT:Q90913; UNIPROT:Q9090:
R;Komine, Y.; Maita, T.; Matsuda, G.
J. Biochem. 110, 60-67, 1991
                                                                                                                                                                                                                                                           A;Title: The primary structure of skeletal muscle myosin A;Reference number: PX0050; MUID:92041767; PMID:1939027 A;Accession: PX0050
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                                                                                                                                                        A; Molecule type: protein A; Residues: 1-205 < HAY>
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C;Species: Oncorhynchus mykiss (rainbow trout)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEKETPVQKCQRLQIEMNELLNEVAALQVDRKVA--DEE----KQSYDAVVATVIST 51
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Pred. No. 24;
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Pred. No. 2
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A;Title: The primary structure of skeletal muscle myosin heavy chain: II. A;Reference number: PX0051; MUID:92041768; PMID:1939028 A;Accession: PX0051

Sequence of

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A; Molecule type: protein A; Residues: 206-636 < KOM>

Matsuzono,

K.; Tanioka,

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Matsuda,

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A; Molecule type: protein
A; Residues: 852-906, 'Q. '908-1108 <WA2>
R; Residues: 852-906, 'Q. '908-1108 in. T.; Hayashida, M.
R; Matteuda, G.; Maita, T.; Miyanishi, T.; Hayashida, M.
J. Protein Chem. 6, 33-46, 1987
A; Title: Structure and function of muscle myosin.
A; Reference number: A60877
A; Reference number: A60877
A; Accession: A60877
A; Molecule type: protein
A; Residues: 1-139,141-205 <WA1>
R; Gulick, J.; Kropp, K.; Robbins, J.
J. Biol. Chem. 260, 14513-14520, 1985
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A,Title: Study on tail region
A;Reference number: PW0009
A;Accession: PW0009
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. Hoppe-Seyler 370, 549-558, 1989
A;Title: Amino-acid sequence of the short subfragment-2
A;Reference number: S04501; MUID:89374803; PMID:2775482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Moore, L.A.; Arrizubleta, M.J.; Tidyman, W.B.; Herman, L.A.; B3
J. Mol. Biol. 225, 1143-1151, 1992
A;Tille: Analysis of the chicken fast myosin heavy chain family.
A;Reference number: S24348; MUID:92309413; PMID:1377278
A;Accession: S24351
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A;Title: The primary structure of the myosin head.
A;Reference number: A26365; MUID:87092420; PMID:3467365
A;Accession: A26365
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A;Title: Complete amino-acid sequence of subfragment-2
A;Reference number: S05515; MUID:90121764; PMID:2610940
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A;Residues: 1082-1182_'T',1184-1203,'DV',1206-1342,'E',1344-1544,'S',1546-1780,'M',1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1081-1203,'DV',1206-1342,'E',1344-1544,'S',1546-1795,'HV',1798-1829,'S',183
A;Cross-references: EMBL:M74084
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3iol. Chem. Hoppe-Seyler 370, 55-61, 1989
3iol. Chem. Hoppe-Seyler 370, 55-61, 1989
3;Title: Amino-acid sequence of the hinge region in chicken A;Reference number: S02082; MUID:89228549; PMID:2713098
A;Accession: S02082
A;Accession: S02082
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A; Residues: 833-1938 < MA2>
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;Maita, T.; Yajima, B.; Nagata, S.; Miyanishi, T.; Nakayama,
. Biochem. 110, 75-87, 1991
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on of skeletal muscle myosin;
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A;Accession: C25217
A;Molecule type: DNA
A;Molecule
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-J
C;Accession: F64596
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.;
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bow
Nature 389, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smi
A;Title: The complete genome sequence of the gastric pathogen Helico
A;Reference number: A64520; MUID:97394467; PMID:9252185
A.ccession: F64596
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F;1290-1938/Region: light meromyosin
F;1290-1938/Region: light meromyosin
F;12/Modified site: acetylated amino end (Ala) #status experimental
F;35/Modified site: N6-methyllysine (Lys) #status experimental
F;35/Modified site: N6,N6,N6-K6-trimethyllysine (Lys) #status ex
F;185/Binding site: ATP (Lys) #status predicted
F;185/Bounding site: ATP (Lys) #status predicted
F;697,707/Active site: Cys #status predicted
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A;Title: A canonical sequence organization
A;Reference number: A92587; MUID:86196091;
                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-111 <TOM>
A; Cross-references: UNIPROT:025335;
C; Superfamily: Helicobacter pylori !
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                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not
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A; Residues: 'M', 1-168 <GUL>
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18; Conserv
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Pred. No. 71;
13; Mismatches
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Pred. No.
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protein jhp0557
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M.; Fujii, C.; Bowman, C.; Watthe
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C;Accession: A59293
R;Macda, K.; Hostinova, B.; Roesc.Kleinkauf, A.; Schuster, H.; Gasperik, J.; Wittinghofe submitted to GenBank, July 1995
A;Description: Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEASAUR 13
S24348 myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Feh-1004 #------
             A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mkNA
A;Residues: 1-1938 <MAE>
A;Rross-references: UNIPROT:Q28641; GB:U32574; NID:g940232; PIDN:AAA74199.1; PID:g94023
A;Experimental source: strain New Zealand White; cell type skeletal muscle fiber type I
                                                                                                                                                                                                                                                                                                    skeletal myosin heavy chain - domestic rabbit
C;Species: Oryctolagus cuniculus
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9DGM5; EMBL:M74085
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E. J. Mol. Biol. 225, 1143-1151, 1992
A;Title: Analysis of the chicken fast myosin heavy chain family. Localizat
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Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L.A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Status: preliminary
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A; Residues: 1-222 <STO>
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-230 <GLA>
À, Gross-references: UNIPROT: 08Y927; GB:NC_003210; PIDN: CAC98793.1; PID: g16410104; GSPDB: 14 A) Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                              .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
Science 294, 849-852, 2001
A, Atthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Malok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.
A, Reference number: AB1077; MUID:21537279; PMID:11679669
A, Accession: AC1164
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                                                                                                                                               A;Gene: lmo0715
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C;Species: Listeria monocytogenes
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C; Accession: AC1164
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Q9ydx9
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Q9ptg6 gallus gall
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9 aeropyrum p
7 aquifex aeo
2 xenopus lae
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schizosacch
chlamydia m
                       spironucleu
oncorhynchu
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sulfolobus
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           rana catesb
                                                                       arabidopsis
                                                                                                                   rana catesb
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Q9V4Y9
Q9V4Y9;
01-MAY-2000
01-MAY-2000
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01-MAY-2000 (TrEMBLrel. 13,
25-OCT-2004 (TrEMBLrel. 28,
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Name=Dmn; ORFNames=CG8269;
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ALIGNMENTS	WYSS_CHICK MYH2_HUMAN Q86T56 Q7REL0 Q25335 Q25335 Q983X1 Q46317 Q46317 Q9REY3 Q9REW6 Q9REW6 Q9ESW6 Q9ESW6 Q9ESW6 Q9ESW6 Q7RT66	
	P13538 gallus gall O9ukx2 homo sapien O86t56 homo sapien O7rel0 plasmodium O25335 helicobacte O983x1 rhizobium l O46317 carnobacter O9rey3 carnobacter O71iu8 lactobacill O9hq83 halobacteri O9esw6 mus musculu O63939 rattus gp. P87344 theragra ch O7rt66 plasmodium	

PRELIMINARY;

380 A

Last sequence update)

update)

Created)

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Randell M.D., Zhang Q., Chen L.X., RA Wan K.H., Doyle C., Baxter E.G., Hell G., Nelson C.R., Gabor G.L., RA Wan K.H., Doyle C., Baxter E.G., Hell G., Nelson C.R., Gabor G.L., RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., RA Ballew R.M., Basu A., Baxter E.G., Hell G., Nelson C.R., Gabor G.L., RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davemport I.B., Davies P., RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C., RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Mount S.M., Pittman G.S., Pan S., Pacleb J.M., Nelson D.L., RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shieh H., RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., RA Raiser R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Harly K., Weinston M., Weinston M., Weinstoh J., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaver J., Zhann M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.M., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. MEDLINE=20196006; SEQUENCE FROM N.A. NCBI_TaxID=7227; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

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Best Local
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlsor Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Ge Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Munge Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong : Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB003835; AAF59034.1; -.
EMBL; AB003835; AAF59034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Murny D.M., Nelson C.R., Pacleb J.M., Park S., Ffeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Wyers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINB=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                SEQUENCE
                                                                                                                                                           FlyBase; FBgn0021825; Dmn.
GO; GO:000586; C:dynactin complex;
GO; GO:0007017; Pimicrotubule-based
InterPro; IPR006996; Dynamitin.
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426070; PubMed=12537573;
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                                                                52;
                                                                               Similarity
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                  GEKETPVQKCQRLQIEMNELLNEVAALQVDRKVADEEKQSYDAVVATVISTAR
GEKETPVQKCQRLQIEMNELLNEVAALQVDRKVADEEKQSYDA-VATVISTAR
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Pred. No. 1e-1
0; Mismatches
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                                                                                                                                                                             process; IEA
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Miranda A., Mungall C.J.,
Phouanenavong S., Wan K.,
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Q9PTG6;
01-MAY-2000
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SEQUENCE
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Schroer T.A., Gill S.R., Hasbani J., Crego C.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
EMBL; AF200744; AAF13996.1; -.
GO; GO:0005869; C:dynactin complex; IEA.
GO; GO:0007017; P:microtubule-based process; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neonhera: Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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Q7PZ25;
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MEDLINE=2005693; PubMed=10588646;

Waletti C., Wetzel D.M., Schrader M.,

Kreis T.E., Schroer T.A.;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
-i- CAUTION: The sequence shown here is derived from an
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Name=agCG52050;
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01-MAR-2004
                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             overexpression and colocalization Mol. Biol. Cell 10:4107-4120(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Role of dynactin in endocytic traffic: effects of overexpression and colocalization with CLIP-170.";
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Pfam; PF04912; Dynamitin; 1.
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                                                                                                                      Pro; IPR006996; Dynamitin.
PF04912; Dynamitin; 1.
NCE 402 AA; 45126 MW: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
6:
Score 82; DB
Pred. No. 0.86
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 127.5; DB 2
Pred. No. 7.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4F5A549B51D52555 CRC64;
                                                                                                                                F229C467C630DCB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hasbani M.J.,
                              0.86;
                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
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                                                                                                                                                                                                                                  ΙEΑ
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   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                databases
                                                            Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
   Indels
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Best Local (
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           Q7T3H1;
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PubMed=15263089; DOI=10.1073/pnas.0402424101;

Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,

Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,

Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,

Praser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertzak H.,

Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,

Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;

"Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               О6СХКТ
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum). Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similar to dynactin 2 (P50).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004)
EMBL; BX950851; CAG77401.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacteriaceae; Pectobacterium.
CBI_TaxID=29471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=ECA4506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORFNames=zgc:63867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factors."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.8%;
40.9%;
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28,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 77; DB 2; Length 242; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A67C186B12E6240C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
   Garcia A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242
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                                                                                                                                                                     RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., KoEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Schautz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;
"Generation and intitial analysis of more than 15 No. 5malts D.E.,
"Generation and intitial analysis of more than 15 No. 5malts D.E.,
"Generation and intitial analysis of more than 15 No. 5malts D.E.,
"Generation and intitial analysis of more than 15 No. 5malts D.E.,
"Generation and intitial analysis of more than 15 No. 5malts D.E.,
"Generation and intitial analysis of more than 15 No. 5malts D.E.,
"Generation and intitial analysis of more than 15 No. 5malts D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Dynactin complex 50 kDa subunit (50 kDa dynei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DCT2_MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC053120; AAH53120.1; -. ZFIN; ZDB-GENE-040426-1279; zgc:63867. GO; GO:0005869; C:dynactin complex; IEA. GO; GO:0007017; P:microtubule-based process;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (p50 dynamitin) (DCTN-50) (Dynactin 23-48K) (GMP23-48K).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Dctn2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.;
                                    SEQUENCE OF
                                                                                                                              and mouse
                                                                                                                                                        "Generation and initial analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006996; Dynamitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF04912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVKETPQQKYQRLVNEIHELCQDVEKIQTSTKESGAEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEKETPVQKCQRLQIEMNELLNEVAALQVDRKVADEEKQ
                                                                                                                              cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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                                 65-74;
   LOCATION,
                                                                                            Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                            Sci. U.S.A.
                                 77-91;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44625 MW;
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   102-116; 156-170; 194-216
DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 75; 1
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA00047342500953 CRC64;
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                                                                                                                                                           of more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kDa dynein-associated polypeptide)
2) (Growth cone membrane protein
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                                    AND 309-320
                                                                                                                                                           full-length human
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RESULT
Q6AYH5
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Best Local :
                                                                                                                                                                                                                                                    Q6AYH5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97289622; PubMed=9144527; DOI=10.1006/bbrc.1997.6447; Abe T.K., Tanaka H., Iwanaga T., Odani S., Kuwano R.; "The presence of the 50-kDa subunit of dynactin complex in the nerve growth cone."; Biochem. Biophys. Res. Commun. 233:295-299(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INIT MET
PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Klausner R.D., Collins F.S., Wagner L., Shenn Altschul S.F., Zeeberg B., Buetow K.H., Schae
                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                TISSUE=Testis;
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                           Name=Dctn2;
                                                                                                                                                                                                       25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                       25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dynactin pathway by interacting with these EMBO J. 20:4041-4054(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21376652; PubMed-11483508; DOI=10.1093/emboj/20.15.4041; Hoogenraad C.C., Akhmanova A., Howell S.A., Dortland B.R., de Zeeuw C.I., Willemsen R., Visser P., Grosveld F., Galjart N.; "Mammalian Golgi-associated Bicaudal-D2 functions in the dynein-
                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH BICD2
                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buropean Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for contites requires a license agreement (See http://www.isb-sib.ch/asend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Subunit of dynactin, a multiprotein complex associated with dynein (By similarity). Interacts with BICD2.
SUBCELLULAR IOCATION: Cytoplasmic and membrane-associated.
DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and plays a role in prometaphase chromosome alignment and organization during mitosis. May play a role in synapse for during brain development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Modulates cytoplasmic dynein binding to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated form are greatly reduced in the adult.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and membrane-associated forms in neonates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:107733; Dctn2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF04912;
                                                                                                                                                                                                                                                                                                                                                    93
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                                                                                                                                                                                           'n
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                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                            GEKETPVOKCORLOIEMNELLNEVAALQVDRKVADEEKQSYDAVVATVISTAR
                                                                                                                                                                                                                                                                                                                                                GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVVLAKQLAALK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microtubule; Motor protein.

0 By similarity.
98 131 Colled coil (Potential).
214 244 Colled coil (Potential).
401 AA; 43985 MW; 1535E4ABD5940EBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR006996; Dynamitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
214
401
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llarity 35.8%;
Conservative 1
                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                    PRELIMINARY;
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Cytoskeleton; Direct
                                                                                                                                                                                                       28,
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                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                           Score 74; DB
Pred. No. 6.6;
Nismatches
                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein sequencing; Dynein;
                                                                                                                                                                                                                                                                    402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                           6.6;
   Shenmen C.M., Schuler G.D Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nctions in the dynein-
complexes.";
                 Derge J.G.
                                                                                                                                                                                                                                                                                                                                                                                                            24;
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                                                                                                                                                                                                                                                                                                                                                                               53
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RESULT
Q66J30
       PRADA RAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q66J30;
Q66J30;
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rodriguez A.C., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
PubMed=12477332; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Director MGC Project;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC079042; AAH79042.1; -.
GO; GO:0005869; C:dynactin complex; IEA.
GO; GO:0007017; P:microtubule-based process; IEA.
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                "Genetic and genomic tools initiative.";
                                                                                                                                                                                                                                                              Richardson P.;
                                                                                                                                                                                                                                                                                              MEDLINE=22341132;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=MGC82128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGC82128
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25-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                              initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF04912; Dynamitin; NCE 402 AA; 44148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEKETPVQKCQRLQIEMNELLNEVAALQVDRKVADEEKQSYDAVVATVISTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVKETPQOKYORLLHEVQELTTEVEKIKTTVKESATEEKLTPVVLAKQLAALK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR006996; Dynamitin.
                                                                                                                                                                                                            225:384-391 (2002)
                                                                                                                                                                                                                                                                            Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sci.
                                                                                                                                                                                                                                                                          PubMed=12454917; DOI=10.1002/dvdy.10174;
sberg R.L., Wagner L., Pontius J., Clifton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44148 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.7%;
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28,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 74; DB
Pred. No. 6.7;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99:16899-16903 (2002)
                                                                                                                                                                                                                                            Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403
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                                                                                                                                                                                                                                              research:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                              The NIH Xenopus
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DCT2_HUMAN
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TISSUE=Placenta, Skin, and Uterus;

NEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,

RX Altschul S.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Altschul S.B., Wodin T.B., Toshiyuki S., Carninci P., Prange C.J.,

RX Altschul S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Altschul S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Altschul S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Altschul S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Altschul S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Altschul S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Altschul S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

RX Altschul S., Worley N., Sodergren E.J., Lu X., Gibbs R.A.,

RX Altschul S., Touchman J.W., Green E.D., Dickson M.C.,

RX Altschul S., Ketteman M.J., Wyers R.M.,

RX Altschul S., Ketteman M.J., Schmutz J., Myers R.M.,

RX Altschul S.S., Kormun J.W., Green E.D., Dickson M.C.,

RX Altschul S.S., Ketteman M.J., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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Q13561; Q86Y
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] [1] SEQUENCE.
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-96178072; PubMed-8647893; DOI=10.1083/jcb.132.4.617;
MEDLINE-96178072; PubMed-8647893; DOI=10.1083/jcb.132.4.617;
Echeverri C.J., Paschal B.M., Vaughan K.T., Vallee R.B.;
Echeverri C.J., Paschal B.M., Vaughan K.T., Vallee R.B.;
"Molecular characterization of the 50-kD subunit of dynactin "Molecular characterization" of the 50-kD subunit of dynacterization of the 50-kD subunit of 
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Pfam; PF04912;
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01-NOV-1997 (Rel. 35, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Dynactin complex 50 kDa subunit (50 kDa dynein-associated (p50 dynamitin) (DCTN-50) (Dynactin 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Gerhard D.S.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC081081; AAH81081.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for the complex in chromosome tion during mitosis."; Biol. 132:617-633(1996).
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403 AA; 44737 MW; 86BE8CEE54325EF3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sci.
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Pred. No. 7.6;
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Best Local
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CONFLICT
                                                                                                                                                                                            Membrane;
INIT_MET
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U50733; AAC50423.1; --
EMBL; BC000718; AAH00718.1; --
EMBL; BC009468; AAH09468.1; --
EMBL; BC014083; AAH14083.1; --
EMBL; AY189155; AAO34395.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as modified and this statement is not removed. Usentities requires a license agreement (See htt
                                                                                                                                                                                                                                                                                MIM; 607376; -.
GO; GO:0005813; C:centrosome; TAS.
GO; GO:0005869; C:dynactin complex; TAS.
GO; GO:0000776; C:kinetochore; TAS.
GO; GO:0008283; P:cell proliferation; TA
GO; GO:0007067; P:mitosis; TAS.
                                                                                                          SEQUENCE
                                                                                                                                                                  DOMAIN
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                         Coiled coil;
                                                                                                                                                                                                                                                     Pfam; PF04912; Dynamitin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810; Gevaert K., Goethals M., Martens L., Van Damme J., Sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-384 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,00 and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                     InterPro; IPR006996; Dynamitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas G.R., Vandekerckhove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22608298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Platelet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aumais J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biotechnol. 21:566-569(2003). PUNCTION: Modulates cytoplasmic dynein binding to an organelle, and plays a role in prometaphase chromosome alignment and spindle organization during mitosis. May play a role in synapse formation during brain development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Subunit of dynactin, a multiprotein complex associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
 93
                                                                                                                                                                                                                                                                                                                                                                   HGNC:2712; DCTN2.
                                                    19;
                                                                Similarity
                       GEKETPVQKCQRLQIEMNELLNEVAALQVD-RKVADEEK
GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEK
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400
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dynactin subunit,
                                                                                                                                                                                                                                      Cytoskeleton;
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243
398
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35,
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                                                              28.1%;
48.7%;
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                                                                                                                                                                                                                                      Direct protein
                                                                                                                    Coiled coil (Potential).
Coiled coil (Potential).
Coiled coil (Potential).
A -> AFAQEL (in Ref. 1).
E -> ELE (in Ref. 3).
LATV -> PGHS (in Ref. 3).
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Pred. No. 9.7;
                                                                                                                                                                                                                       protein.
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                                                    Mismatches
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                                                                             DB 1;
                                                                                                                                                                                                                                       sequencing; Dynein;
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RESULT 10 Q6IRB3 ID Q6IRB AC Q6IRB

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RESULT 11
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ID Q9LNM
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Dank C., Schmutz J., Myers R.M., Schein J.E.
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Matches
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                                                                       Q9LNM1;
Q9LNM1;
01-OCT-2000
01-OCT-2000
01-MAR-2004
F12K21.7.
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Xenopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S., Strausberg R.; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
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Dctn2-prov protein.
Name=dctn2-prov;
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                                            Arabidopsis
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GO; GO:0005869; C:dynactin complex;
GO; GO:0007017; P:microtubule-based
InterPro; IPR006996; Dynamitin.
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                                            thaliana
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AA; 44828
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51.3%;
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Pred. No. 1
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Best Local :
Query Match
Best Local Similarity
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                                                                                                                      thyroid hormone-induced metamorphosing Ra
Dev. Genet. 24.151-164(1999).
EMBL; AF097904; AAD13769.1; -.
HSSP; P25054; IDEB.
GO; GO:0016459; C:myosin; IEA.
GO; GO:0001774; F:motor activity; IEA.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR00533; Tropomyosin.
Pfam; PF01576; Myosin_tail_1; 1.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hop Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Ryuyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspie Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC023279; AAF79274.1; -. EMBL; AC023279; AAF79274.1; -. EMBL; AC023279; MYB 1; UNKNOWN 1. SEQUENCE 755 AA; 83720 MW; BADBCB41020E022A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, La
01-MAR-2004 (TrEMBLrel. 26, La
Myosin heavy chain (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Tail muscle;
MEDLINE=99179235; PubMed=10079518;
DOI=10.1002/(SICI)1520-6408(1999)24:1/2<151::AID-DVG14>3.3.CO;2-W;
Hu H., Merrifield P., Atkinson B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S Kim C., Altafi H., Bei Q., Chin C., Ciou J., Choi E., Comn L., Kim G., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Com L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J Conway A., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
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01-MAY-1999
                                                                               SEQUENCE
                                                                                                           NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8400;
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                                                                                                                                                                                                                                                                                                                                                                                                 "Expression of the myosin heavy chain genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            582
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                                                                               879
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(TrEMBLrel. 10,
(TrEMBLrel. 26,
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                                                                               101710 MW;
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38.5%;
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27.3%;
36.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70.5; Depred. No. 31; 9; Mismatches
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Score 70.5
Pred. No.
                                                                               1C456851E968A3D8
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                                                                                                                                                                                                                                                                                                                                                                         in the tail muscle of catesbeiana tadpoles.";
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                        Length 879;
                                                                               CRC64;
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Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson-Hopson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Southwick A., Federspiel N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         755;
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RESULT 13
RMYH8_HUMAN
ID MYH88
AC 91353
DT 101-UJ
DT 15-UJ
DT 15-U
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P13535; Q14910;
01-JAN-1990 (Rel. 13, 0
15-JUL-1998 (Rel. 36, 1
25-JAN-2005 (Rel. 46, 1
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Mabry C.C., Lefaivre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95324556; PubMed=7601129;
Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino
Stedman H.H., Rubinstein N.A.;
                                                                                                                                                                                                                                                                                                                                                                                         "Isolation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human perinatal myosin heavy chain.";
J. Cell Biol. 108:1791-1797(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                   PubMed=15282353;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feghali R., Leinwand L.A.;
"Molecular genetic characterization of a developmentally regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90235862; PubMed=1691980;
Bober E., Buchberger-Seidl A., Braun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 502-1937 FROM N.A.
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MEDLINE=90323631; PubMed=2373371; DOI=10.1016/0378-1119(90)90020-R;
Karsch-Mirachi I., Feghali R., Shows T.B. Jr., Leinwand L.A.;
"Generation of a full-length human perinatal myosin heavy-chain-
                                                                                                                                                 complex variant."
                                                                                                                                                                       "Mutation of perinatal myosin heavy chain associated with a Carney
                                                                                                                                                                                                                                                                                                               VARIANT CARNEY COMPLEX VARIANT/TRISMUS-PSEUDOCAMPTODACTYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89234168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of three developmentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skeletal muscle;
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FUNCTION: Muscle contraction.

SUBUNIT: Muscle myosin is a hexameric protein that consists heavy chain subunits (MfC), 2 alkali light chain subunits (MfC-2), and 2 regulatory light chain subunits (MfC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
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. Biochem.
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                                                                                                                                                                                                                                                                                                                                                              Tidhar A., Myszkowski M.;
n and characterization of the human |
(MAY-1998) to the EMBL/GenBank/DDBJ
                                                                                                                             Med.
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                                                                                                                                                                                                                 Bressan M., Mo
faivre J.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                DOI=10.1056/NEJMoa040584;
                                                                                                                         351:460-469(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of a human perinatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=2715179; DOI=10.1083/jcb.108.5.1791;
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                                                                                                                                                                                                                                             McDermott
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A., Destree A., (
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T.,
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                                                                                                                                                                                                                                                                                                                                                                                     perinatal MHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                 Morton C.C
dron J.-M.,
                                                                                                                                                                                                                                                                                                                  SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                     promoter.";
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remailial cardiac myxomas are associated with spotty pigmentation of the skin and other phenotypes, including primary pigmented nodular adrenocortical dysplasia, extracardiac (frequently cutaneous) myxomas, schwannomas, and pituitary, thyroid, testicular, bone, ovarian, and breast tumors. Cardiac myxomas do not develop in all patients with the carney complex, but affected patients have at least two features of the complex or one feature and a clinically significant family history.

-IDISEASE: Defects in MYH8 are a cause of trismus-pseudocamptodactyly syndrome [MIM:158300]; also called Hecht-Beals or Dutch-Kentucky syndrome. The trismus-pseudocamptodactyly in which wrist dorsiflexion, but not volarflexion, produces involuntary fixxion contracture of distal and proximal interphalangeal jointa; Such hand and jaw contractures are caused by shortened flexor muscle-tendon units. Similar lower-limb contractures also produce foot deformity. The trismus-pseudocamptodactyly syndrome is a morbid autosomal dominant trait with variable expressivity but high penetrance. In these patients, trismus complicates dental care, feeding during infancy, and incubation for anesthesia, and the pseudocamptodactyly impairs manual dexterity, with consequent correction of contractures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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DISEASE: Defects in MYH8 are a cause of Carney complex variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subfragment (S2).
SIMILARITY: Contains 1 IQ domain.
SIMILARITY: Contains 1 myosin-like globular head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       correction of contractures.

MISCELLANEOUS: Each myosin heavy chain can meromyosin (LMM) and 1 heavy meromyosin (EAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [MIM:608837]. Carney complex variant characterized by spotty skin pigmentation, cardiac and other myxomas, endocrine tumors, and psammomatous melanotic schwannomas Familial cardiac myxomas are associated with access to the complex variant process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               split further into 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             globular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subfragments
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Actin-binding; ATP-binding; Calmodulin-binding; Coiled coil; Disease mutation; Methylation; Multigene family; Muscle prot. Myosin; Thick filament. InterPro; IPR002928; Myosin_tail Pfam; PP00612; IQ; 1.
Pfam; PP00063; Myosin_head; 1.
Pfam; PP02736; Myosin_N; 1.
Pfam; PP01576; Myosin_tail_1; 1.
PRINTS; PR00193; MYOSINHEAVY. InterPro; IPR000048; IO_region.
InterPro; IPR001609; Myosin_Nea
InterPro; IPR004009; Myosin_N. EMBL; M36769; AAC17185.1; -.
EMBL; Z38133; CAA86293.1; -.
EMBL; X51592; CAA35941.1; -. GO; GO:0005859; C:muscle myosin; TAS.
GO; GO:0008307; F:structural constituent of muscle; TAS MIM; EMBL; AF067143; AAC21557.1; PIR; 138055; 138055. HSSP; P13538; 2MYS. ProDom; PD000355; Myosin_head; 1. PROSITE; PS50096; IQ; 1. Genew; HGNC:7578; 158300; 160741; -. MYH8. ; Myosin_head. ; Myosin_N. ; Myosin_tail. protein;

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Best Local Similarity
Matches 22; Conser
Query Match
Best Local Similarity
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Q92DT9;
01-DEC-2001
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MEDLINE-21537279; PubMed=11679669; DOI=10.1126/science.1063447;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Clakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Berral G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Sindes N., Tierrez A.,

Verenze-Polard J., Nother C., Sindes N., Tierrez A.,

Verenze-Polard J., Nother C., Sindes N., Tierrez A.,
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MOD_RES
VARIANT
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                    EMBL;
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                                                              ListiList; LIN0723; Complete proteome. SEQUENCE 230 AA;
                                                                                                                                  PIR; AC1523; AC1523.
                                                                                                                                                                             Science
                                                                                                                                                                                               Vazquez-Boland J.-A., Voss H., Weh
"Comparative genomics of Listeria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1642;
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                                                                                                                                                    Ce 294:849-852(2001).
AL596166; CAC95955.1; -.
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  26.9%;
30.5%;
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E -> Q (in Ref. 1 and 4).
M -> N (in Ref. 3).
N -> H (in Ref. 1 and 4).
MC -> DGG (in Ref. 3).
E -> G (in Ref. 1 and 4).
K -> Q (in Ref. 1 and 4).
KY -> NT (in Ref. 3).
EN -> AH (in Ref. 3).
EN -> AH (in Ref. 1 and 4).
E -> D (in Ref. 1 and 4).
E -> D (in Ref. 1 and 4).
E -> D (in Ref. 2).
D -> H (in Ref. 2).
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Last annotation updat
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Pred. No. 80;
.5; Mismatches
  Score 69.5;
Pred. No. 12;
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R -> Q (in Carney complex variant and
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                                                                                                                                                                                            T., Simoes N., Tierrez A.,
Wehland J., Cossart P.;
ria species.";
                                                                   05ACFFEB3B38B71D CRC64;
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                        DB
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                      Length 230;
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Search completed: Job time : 95.246
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01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99310339; PubMed=10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., I Hosoyama A., Pukui S., Nagai Y., Nishijima K., Nakazawa H., Takaniya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seg
01-UNN-2003 (TrEMBLrel. 24, Last ann
Hypothetical protein APE0790.
OrderedLocusNames=APE0790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9YDX9
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HSSP; O15813; 1D7M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Desulfurococcaceae; Aeropyrum.
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  November
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                            2005,
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                                                                                                                                                                                                                        Score 68; DB
Pred. No. 23;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                   l protein.
CBBFF3961063E5B8 CRC64;
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Ankai A., no.
                                                                                                                                                                                                                                                                            Length 297;
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-080-897-55-1
US-08-899-595-1
US-08-899-591A-23627
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
19287, A	14143, A	8134, Ap	6417, Ap	21559, A	1, Appli	26, Appl	30, Appl	28, Appl	32, Appl	66, Appl	10668, A	141, App	60196, A	43234, A	58576, A	2, Appli	2, Appli

ALIGNMENTS

RESULT 1 US-09-270-767-43370

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CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURAPATS eqFormatter Version 0.9
SEQ ID NO 918
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43370
LENGTH: 142
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Best Local Similarity
Matches 32; Conservat
                                                                                                                                                                                                                                                                                                            APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes
FILE REFERENCE: 15966-542
                            ORGANISM: Homo sapiens FEATURE:
                                                                     LENGTH: 1937
TYPE: PRT
NAME/KEY: misc_feature
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SEQ ID NO 11104
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Patent No. 6812339
GENERAL INFORMATION:
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APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
SOFTWARE: CURAPATSeqFormatter Version 0.9
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                                                                                                                                                                                                            TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                    PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P12882
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1588 QLKRNHTRVVETMQST 1603
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32.7%; Pred. No. 15;
Live 14; Mismatches
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Pred. No. 1.1;
15; Mismatches 8;
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OF DETECTION
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; ORGANISM: Human
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US-09-949-016-8135
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US-09-949-016-6925
                                                                                                                                  FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 6925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6812339
GENERAL INFORMATION:
                                                        SEQ ID NO 8135
LENGTH: 1942
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8135, Ap
Patent No. 681233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-10-03
                                                                                                SOFTWARE:
                                                                                                                     NUMBER OF SEQ ID NOS:
                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1561 KILRIQLELNQVKSE-----VDRKIAEKDEEIDQMKRNHIRIVESMQST 1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 KCORLOIEMNELLNEVAALQVDRKVA-----DEEKQSYDAVVATVIST
                                                                                              FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09949016
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36.7%;
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                                                                                                                       207012
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Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62.5;
Pred. No. 15
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OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1939;
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                                                                                               ; ORGANISM: Human
US-09-949-016-8888
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P11055
US-09-538-092-901
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Query Match
Best Local Similarity 35.4
Matches 17; Conservative
                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8888, Application US/09949016 Patent No. 6812339
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LENGTH: 1940
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APPLICANT: Mansfield, Traci A.
IITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 1999-04-01
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CLOO1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/178,965 PRIOR FILING DATE: 2000-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.1%; Score 59.5; 1
Local Similarity 35.4%; Pred. No. 40;
Les 17; Conservative 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1564 KILRIQLELNOVKSE-----IDRKIAEKDEELDQLKRNHLRVVESMQST 1607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                  ; Score 59.5; D; Pred. No. 41; 11; Mismatches
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                                                      Length 1963;
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                    Indels
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                Gaps
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RESULT 10
US-09-323-735-2
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                                                                                                                                                           Sequence 2, Application US/09323735
Patent No. 6197932
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                       Query Match
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GENERAL INFORMATION:
APPLICANT: King, N
APPLICANT: Lynch,
                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (650) 343-4342 INFORMATION FOR SEQ ID NO:
                                                         APPLICANT:
APPLICANT:
APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri E.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,897
                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                  2 EKETPVQKCQRLQIEMNELLNEVAALQVDRKVADEEKQSYDAVVATV 48
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                                                                                                                                                                                                                                                                    EKQQIATEKQDLEABVSQLTGEVAKLTKELEDAKKEMASLSAAAITV 563
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Welcsh, Piri L.
Leon, Pedro E.
                                                                                                          King, Mary-Claire
Lynch, Eric D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                        Lee, Ming
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee,
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34.0%;
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                                                                                                                                                                                                                                                                                                                                                       Score 58; DB Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                      Mismatches
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CORRESPONDENCE ADDRESS:

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US-09-080-897-4
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Patent No. 5985574
GENERAL INFORMATI
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/323,735
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/080,897
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 22.5%;
Local Similarity 34.0%;
hes 16; Conservative
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TOPOLOGY: linear
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW
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CLASSIFICATION:
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STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                              COUNTRY:
                                                           FILING DATE:
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; Pred. No. 37;
9; Mismatches
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                                                          US-08-899-595-1
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US-08-899-595-1
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Patent No. 6111072
                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-UUL-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: UP 8-242701
FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 9-90170
FILING DATE: 25-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 049441/0112
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Best Local Similarity
   Query Match
Best Local Similarity
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APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (650) 343-43
INFORMATION FOR SEQ ID NO:
                                                                                                                             INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3000 k st
CITY: Washington
                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                              amino acid
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ilarity 35.8%;
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     22.5%;
35.8%;
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RHO TARGET PROTEIN HUMAN MDIA AND GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENCODING SAME
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     Score 58;
Pred. No.
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DB
37;
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                        Length 1255;
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RESULT 13
US-09-323-735-4
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US-09-323-735-4
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Best Local Similarity
                                                                               Sequence 3, Application US/08899595
Patent No. 6111072
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GENERAL INFORMATION:
APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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75 DENISE DRIVE
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(70 TO NO: 4:
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Welcsh, Piri L.
Leon, Pedro E.
ENTION: Modulators of Actin
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                                                                                                                                                                                                                                             22.5%; Score 58; DB 35.8%; Pred. No. 37; tive 10; Mismatches
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                                                                                                                                                                                                                                                                              DB 3; Length 1255;
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; Sequence 23627, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-899-595-3
                                                                                                                               PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23627
LENGTH: 1413
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MAYC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
Best Local Similarity Matches 17; Conserv
                                    Query Match
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-9017
FILING DATE: 25-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Stephen A. Bent
REGISTRATION NUMBER: 29,768
                                                                                             ORGANISM: Pseudomonas aeruginosa
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-242701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/899,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 24-JUI
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            569 EKQQIATEKQDLEAEVSQLTGEVAKLTKELEDAKKEMASLSAAAITV 615
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Conservative
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              22.5%;
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11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9,
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                  Score 58; DB
Pred. No. 43;
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                                    4;
16;
                                    Length 1413;
Indels
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10;
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Gaps
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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44:
55:
66:
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110:
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258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEKETPVQKCQRLQIEMNEL......ADEEKQSYDAVVATVISTAR 53
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Copyright (c) 1993 - 2005 Compugen Ltd.
            / Cgm2 6/ptodata/1/pubpaa/USO9A PUBCOMB.pep: *
/cgm2 6/ptodata/1/pubpaa/USO9A PUBCOMB.pep: *
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/cgm2 6/ptodata/1/pubpaa/USO9C PUBCOMB.pep: *
/cgm2 6/ptodata/1/pubpaa/USO9C PUBCOMB.pep: *
/cgm2 6/ptodata/1/pubpaa/US10A PUBCOMB.pep: *
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/cgm2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep: *
/cgm2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep: *
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/cgm2 6/ptodata/1/pubpaa/US11 NEW PUB.pep: *
/cgm2 6/ptodata/1/pubpaa/US10 NEW PUB.pep: *
/cgm2 6/ptodata/1/pubpaa/US11 NEW PUB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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81	88	93	98	103	105	108	114	243.5	243.5	258	Score
31.4	34.1	36.0	38.0	39.9	40.7	41.9	44.2	94.4	94.4	100.0	Query Match Length DB
16	17	18	19	20	22	21	22	380	380	53	Length
10	10	10	10	10	10	10	10	20	10	10	DB
US-09-782-816A-32	US-09-782-816A-31	US-09-782-816A-30	US-09-782-816A-29	US-09-782-816A-28	US-09-782-816A-2	US-09-782-816A-27	US-09-782-816A-26	US-11-097-143-4056	US-09-782-816A-56	US-09-782-816A-52	ID
Sequence 32, Appl	Sequence 31, Appl	Sequence 30, Appl				Sequence 27, Appl	Sequence 26, Appl	Sequence 4056, Ap	Sequence 56, Appl	Sequence 52, Appl	Description

RESULT 2
US-09-782-816A-56
; Sequence 56, Application US/09782816A
; Publication No. US20030032771A1

4 5	44	43	42	41	40	39	38	37	36	35	34	သ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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US-10-335-977-8524	08-765	-09-738-630-9	-10-723	-10-408-	-10-767-701-41	-10-732-923-3	0-450-763-51	-10-424-599-1	364	-273	-805-684-15	-401	US-10-205-219-102	-13	364-761-	364-761-3	-10-424-599-	-425-114-	0-42	-10-	-09-78	09-864-761-4	-10-723-860-	-860-	-09-782-816A-3	US-10-102-806-676	09-925-2	9-782-816A	-10-408	US-09-782-816A-51	-10-425-115-3	-09-782-816A-5	Α-
8524	1Ce 1175	e 99, Ap	54,	1655,	41002,	Sequence 3351, Ap	e 51592,	e 170		26,	152	218	102	e 134	42193,	39043,	20706	48404,	20707	3311	e 35, Aj	43401,	106,	58,	34,	e 676,	676	e 53,	e 136	e 51,	e 319	e 54,	w

ALIGNMENTS

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US-09-782-816A-52
                                                                                                                                           US-09-782-816A-52
                                                                                                                                                                                            FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52
LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 52, Application US/09782816A Publication No. US20030032771A1 GENERAL INFORMATION:
                                                                      Matches
                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                 APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                 LENGTH: 53
TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                     Local Similarity
                                                                      53;
100.0%; Score 258; DB 10; illarity 100.0%; Pred. No. 1.9e-25; Conservative 0; Mismatches 0;
                                                                      Indels
                                                                                                      Length
                                                                    ٥,
                                                                    Gaps
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APPLICANT: Venter, J. Craig

APPLICANT: et al.

FITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOO0728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 1999-10-19
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                                                                                                                                                                           ; LENGTH: 380
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-4056
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US-11-097-143-4056
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APPLICANT: ROGERS, Gregory C.

APPLICANT: Scholey, Jonathon M.

APPLICANT: Scholey, Jonathon M.

TITLE OF INVENTION: PEPTIDE INHIBITORS OF CEI

TITLE OF INVENTION: PROLIFERATION

FILE REFERENCE: UC069.001A

CURRENT APPLICATION NUMBER: US/09/782,816A

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 380
TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                      SEQ ID NO 4056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Publication No. US20050208558A1
                                                                                     Matches
                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                        PRIOR PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FASTSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/161,932 PRIOR FILING DATE: 1999-10-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/173,383
FILING DATE: 1999-12-28
APPLICATION NUMBER: 60/175,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/164,769
FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-01-12
APPLICATION NUMBER: 60/184,831
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94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 GEKETPVOKCORLQIEMNELLNEVAALQVDRKVADEEKOSYDA-VATVISTAR 145
                                                                                     52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GEKETPVQXCQRLQIEMNELLNEVAALQVDRKVADEEKQSYDAVVATVISTAR 53
                       GEKETPVQKCQRLQIEMNELLNEVAALQVDRKVADBEKQSYDAVVATVISTAR 53
GEKETPVQKCQRLQIEMNELLNEVAALQVDRKVADEEKQSYDA-VATVISTAR 145
                                                                                     Conservative
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                                                                                                        94.4%;
98.1%;
                                                                               Score 243.5; DB 20;
Pred. No. 1.6e-22;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 243.5; DB 10; Length Pred. No. 1.6e-22; 0; Mismatches 0; Indels
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                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 380;
                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10,000 OR MORE
                                                                                                                               380;
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. RESULT 4

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APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 21
TYPE: PAT
ORGANISM: Drosophila melanogaster
US-09-782-816A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Sharp, David J.

APPLICANT: Rogers, Gregory C.

APPLICANT: Scholey, Jonathon M.

TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR

TITLE OF INVENTION: PROLIFERATION

FILE REFERENCE: UC069.001A

CURRENT APPLICATION NUMBER: US/09/782,816A

CURRENT APPLICATION NUMBER: US/09/782,816A

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 22
Sequence 2, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CEI
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
CURRENT APPLICATION UMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 22
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-782-816A-26
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                                                                                                                                                                                                                                                                      RESULT 6
US-09-782-816A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27, Application US/09782816A Publication No. US20030032771A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sharp, David J. APPLICANT: Rogers, Gregor APPLICANT: Scholey, Jonat
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                                                                                                                                                                                                                                                                                                                                                                                                     2 EKETPVOKCORLOIEMNELLN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.2%; Score 114; DB 10; 100.0%; Pred. No. 1.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 108; DB 10; Pred. No. 9.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                   OF CELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Drosophila melanogaster US-09-782-816A-2
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SEQ ID NO 2
LENGTH: 22
                                                                                                                                                              SEQ ID NO 29
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/09782816A Publication No. US20030032771A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/09782816A Publication No. US20030032771A1
                                                    Matches
                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                  -09-782-816A-29
                                                                                                                                                                                                                                                                APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/782,816A CURRENT FILING DATE: 2001-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                        TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                Local
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les 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KETPVOKCORLOIEMNELLN 22
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                                                                Similarity
ETPVQKCQRLQIEMNELLN 22
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                                                    Conservative
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                                           38.0%; bu
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.9%; Score 103; DB 10; 100.0%; Pred. No. 3.9e-06; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105; DB 10;
; Pred. No. 2.4e-06;
                                                                Score 98;
Pred. No.
                                                    Mismatches
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                                                1.6e-05;
hes 0;
                                                                                DB 10;
                                                                                Length 19;
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APPLICANT: Rogers, Gregory C.

APPLICANT: Scholey, Jonathon M.

TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR

TITLE OF INVENTION: PROLIFERATION

FILE REFERENCE: UC069.001A

CURRENT APPLICATION UMBER: US/09/782,816A

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 18
                                                                                     RESULT 11
US-09-782-816A-32
is Sequence 32, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION
GENERAL INFORMATION
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US-09-782-816A-31
; Sequence 31, Application US/09782816A
; Publication No. US20030032771A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 31
LENGTH: 17
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: ROgers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
PILE REFERENCE: UC069.001A
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Best Local Similarity
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APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                             PVQKCQRLQIEMNELLN
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                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                              34.1%; Score 88; DB 10;
100.0%; Pred. No. 0.00026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.0%; Score 93; 100.0%; Pred. No.
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FILE REFERENCE: UC069.001A

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RESULT 13
US-09-782-816A-54
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                                                       US-09-782-816A-54
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CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
SEQ ID NO 32
TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
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Query Match
Best Local Similarity
                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 183
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local 9
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APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
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CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 15
TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 31.4%;
Local Similarity 100.0%;
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28.7%;
35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.8%; Score 77;
100.0%; Pred. No.
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Pred. No. 0.0019;
 Score 74; DB 10;
Pred. No. 0.32;
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                Length 183;
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APPLICANT: Sharp, David J.

APPLICANT: Rogers, Gregory C.

APPLICANT: Rogers, Gregory C.

APPLICANT: Rogers, Jonathon M.

TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR

TITLE OF INVENTION: PROLIFERATION

FILE REFERENCE: UC069.001A

CURRENT APPLICATION NUMBER: US/09/782,816A

CURRENT APPLICATION NUMBER: US/09/782,816A

CURRENT FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 51

LENGTH: 52
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US-09-782-816A-51
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                                                                                                                                              US-09-782-816A-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 315831
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 315831, Application US Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51, Application US/09782816A Publication No. US20030032771A1
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                          NAME/KEY: UNSURE
LOCATION: 44
OTHER INFORMATION: Xaa = Val or Leu
OTHER INFORMATION: A sequence conse
                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                             OTHER INFORMATION: musculus.
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Unknown
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19; Conservative
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GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEK
                            GEKETPVOKCORLOIEMNELLNEVAALQVD-RKVADEEK 38
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Search completed: November 3, 2005, 22:11:41 Job time: 96.5134 secs

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T49451
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-804 <MUR>
A;Cross-references: UNIPROT:Q95X56; EMBL:AF040659; PIDN:AAB95062.1; GSPDB:GN00019; CESP:A;Experimental source: strain Bristol N2; clone ZK484
C;Genetics:

A;Gene: CESP:ZK484.4

Symuracy, J.; Wohldmann, P.
submitted to the EMBL Data Library, December 1997
submitted to the EMBL Data Control of C. elegans cosmid

ZK484

A; Reference number: A;Description: The sequence A;Reference number: Z21237 hypothetical protein ZK484.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct.1999 #sequence_revision 29-Oct.1999 #text_change 09-Jul-2004 C;Accession: T32864

T32864 RESULT 1

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	50
57.5	Մ 8	58	58	58	58	58	58	58	58	58	58	58.5	58.5	59	27
22.9	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.3	23.3	23.5	60.0
237	2422	2139	978	740	727	707	677	630	623	319	302	821	154	2101	701
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C87656	T12687	T18296	A70387	G95153	AD2188	S78538	T22333	D97992	A48315	T25666	T01615	AI2417	T25602	A42184	140/20
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GGDEF family prote	ALR protein homole	myosin heavy chai	conserved hypothe	neuraminidase, pr	hypothetical p	site-specific reco	histidine ammonia-	hypothetical prote	lamin LII - Afric	hypothetical prote	hypothetical prote	hypothetical prot	hypothetical prote	nuclear mitotic ap	TOTAL TENTOCHER

ALIGNMENTS

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kinesin-like protein Kif2la related protein [imported] - Neurospora crassa N;Alternate names: protein B14D6.30 C;Species: Neurospora crassa C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004 C;Accession: T49451 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1742 <SCH>
A;Cross-references: UNIPROT:QBXOC5; EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.30
A;Experimental source: BAC clone B14D6; strain OR74A
C;Genetics:
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A; Accession: T49451
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A;Introne: 52/1; 113/1; 162/3; 201/3; 248/2; 346/1; 433/2; 464/3; 565/3; 628/2; 646/3; C;Superfamily: Caenorhabditis elegans hypothetical protein ZK484.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n 27.7%; Score 69.5; Similarity 34.4%; Pred. No. 20; 22; Conservative 10; Mismatches
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R;Holzbaur, E.L.F.; Hammarback, J.A.; Paschal, B.M.; Kravit, N.G.; Pfister, K.K.; Vallee Nature 351, 579-583, 1991
A;Title: Homology of a 150K cytoplasmic dynein-associated polypeptide with the Drosophil A;Reference number: S16129; MUID:91260877; PMID:1828535
A;Accession: S16129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
$16129
$16129
Syncin-associated protein, 150K, cytosolic - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
                    FmtB protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence revision 10-May-2001 #text_char
                                                                             D90011
                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1287 <WIL>
A;Cross-references: UNIPROT:062245; EMBL:Z93382; PIDN:CAB07612.1; GSPDB:GN00021; CESP:F4
A;Experimental source: clone F45G2
C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F45G2.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T22235
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A;Molecule type: mRNA
A;Residues: 1-1325 <KKV>
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submitted to the EMBL Data Library,
A;Reference number: Z19535
A;Accession: T22235
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Matches
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Best Local
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;Introns: 59/2; 117/3; 153/3; 180/2; 233/2; 341/3;
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18; Conser
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  D90011
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                                                                                                                                                          EPPPEKRQKILEVIDDDFSEFFQEKVKENTKESVAEEKVENSNEELKPPPILRKAVS 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVKETPOOKYORLLHEVOELTTEVEKIKTTVKESATEEKLTPVLLAKOL 49
                                                                                                                                                                                         ETPQQKYQRLLHEVQELTTEV--EKIKTTVKESATEEKL-----TPVLLAKQLA 50
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                                                                                                                                                                                                                                  26.7%; Score 67; DB llarity 31.6%; Pred. No. 61; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.9%; Score 67.5; I
34.7%; Pred. No. 56;
tive 11; Mismatches
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; Pred. No. 66;
8; Mismatches
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                                                                                                                                                                                                                                                                      DB 2; Length 1287;
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                                                                                                                                                                                                                                    Indels
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Query Match
Best Local Similarity
Thes 17; Conserve
                                                                                                                                                                                                                                                                                                                            R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, submitted to the Protein Sequence Database, the A;Reference number 215391
A;Accession: T04957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seki C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D90011
                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F7J7.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 09-Jul-2004
                                                                                                                                                               A; Introns: 80/1;
A; Note: F7J7.200
                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-393 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-2481 <KUR>
A;Cross-references: UNIPROT:Q99QR6;
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                     A; Map position: 4
                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:049567; EMBL:ALO21960 A;Experimental source: cultivar Columbia; BAC clo
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                                                                                                                                                                                    ;Introns: 80/1; 217/3; 264/1; 291/3
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Best Local Similarity
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    27
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VKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEE 38
                                        KETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEE-KLTPVLL 45
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                                                                                  Conservative
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                                                                                                   26.3%;
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                                                                                                   Score 66; DB Pred. No. 21;
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Pred. No. 1.2e+02;
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                                                                                  Mismatches
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July 1998
                                                                                                                                                                                                                                               clone
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                                                                                                                      Length 393;
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    63
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K.; I
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RESULT 7 C71509 probable DNA polymerase I - Chlamydia trachomatis (serotype D, strain UW3/Cx) C;Species: Chlamydia trachomatis C;Dace: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Ju1-2004 C;Accession: C71509 A; Gene: pola C; Superfamily: C;Accession: C71509

C;Accession: C71509

R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R Science 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen A;Reference number: A71570; MUID:99000809; PMID:9784136

A;Accession: C71509 A; Experimental source: A;Cross-references: UNIPROT:O84500; A;Experimental source: serotype D, : A;Residues: 1-866 <ARN> A; Molecule type: DNA A;Status: preliminary Genetics: DNA-directed DNA polymerase Score 66; ; GB:AE001322; GB:AE001273; NID:g3328916; PIDN:AAC6809 strain UW-3/Cx 멂 2 Length 866; R.; Aravind, L.; of humans: Chlamydia

Mitchell,

traci

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RESULT 10
S69518
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C; Superfamilu...
  hypothetical protein 12 - C;Species: phage HP1 C;Date: 06-Dec-1996 #seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-1837 <MUR>
A;Residues: 1-1837 <MUR>
A;Residues: 1-1837 <MUR>
A;Cross-references: UNIPROT:074424; EMBL:AL023860; PIDN:CAA19588.1; GSPDB:GN00068; SPDB
A:Experimental source: strain 972h-; cosmid c162
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A; Residues: 1-210 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein At2g11890 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 12-Jul-2004 C;Accession: E84499
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A; Accession: T41023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: E84499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Species: Schlzosaccharomyces pombe;Date: 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                    ;Cross-references: UNIPROT:Q9SIY3; GB:AE002093; NID:g4557062; PIDN:AAD22501.1; GSPDB:GN
                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                         Superfamily: uncharacterized CYTH domain protein
                                                                                                                                                                                                                                                                                                                                 Gene: At2g11890
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Best Local
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQKYQRLLHEVQELTTEVEKIKTTV--KESATEEKLTPVLLAK-----QLAAL
                                                                                                                                                              GVK-ETPQQKYQ-RLLHEVQELTTEVEKIKTTVKESATEEKL 40
                                                                                                                                      GVKLEVDETKYDFGNCYEIECETEEPERVKTMIEEFLTEEKI 191
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                                                                                                                                                                                                               25.5%; ilarity 40.5%; Conservative
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llarity 35.8%;
Conservative
#sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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                                        phage HP1
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; Pred. No. 1.3e+02;
10; Mismatches 17
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Pred. No.
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.0; Mismatches
                                                                                                                                                                                                           Pred. No. 17;
9; Mismatches
                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                     Length 210;
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                                                                                                                                    CiAccession: F7521b
R;anonymous, Genoscope
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
submitted to the EMBL Data Library, July 1999
  A;Cross-references: UNIPROT:Q9V217; GB:AJ248283; A;Experimental source: strain Orsay C;Genetics:
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                                                            A; Residues: 1-281 < KAW>
                                                                            A; Molecule type:
                                                                                              A; Status: preliminary
                                                                                                                  A; Accession: F75216
                                                                                                                                  A; Reference number: A75001
                                                                                                                                                                                                                                                                                                           RESULT 12
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                    223 L 223
                                                                                                                                                                                                                                                                                                                                                                                                            52 L 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.3%;
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hypothetical protein aq_1060 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: D70391
                                                                                                  hypothetical protein PAB2181 - Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: aq 1060
C;Superfamily: multidrug resistance protein A; lipoyl/biotin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P51714; EMBL:U24159; NID:g1046235; A;Note: the nucleotide sequence was submitted to the EMBL Data C;Superfamily: phage HP1 hypothetical protein 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Esposito, D.; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, A.S.; Scocca, Nucleic Acids Res. 24, 2360-2368, 1996
A; Title: The complete nucleotide sequence of bacteriophage HP1 DNA.
A; Reference number: S69503; MUID:96279738; PMID:8710508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:067159; GB:AE000721; NID:g2983544; PIDN:AAC07129.1; PID:g298
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-163 <ESP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Deckert, G.; Warren, P.V.; Gaasterland,
                                                                                                                                                                                                                                                                                                                                                                                                           164 PRRKFEEVDTNLKVLLHEREYLEKSIQEINTEIKRAKKGI-ENARNEFKTIEELKKELSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 PQQKYQR-----LLHE-----VQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TPOOKYORLLHEVOELTTEVEKIK-TTVKESATEEKLTPVLLAKO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPQKQFIKLMEEFGELCSGVAKNKPDVIKDSIGDCFVVMVILAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.3%; Score 63.5; Ilarity 37.8%; Pred. No. 15; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
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  insights
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                                                                                                     #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 374;
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  into
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Library, April 1995
                                                                                                          09-Jul-2004
  archaeal chromosome
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GB:AL096836; NID:g5457433;

PIDN:CAB4918

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RESULT 15
T32222
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F90577
hypothetical protein T23B12.7 - C: C; Species: Caenorhabditis elegans
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Biochem. Biophys. Res. Commun. 231, 344-347, 1997
A;Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate for th A;Reference number: JC5368; MUID:97223454; PMID:9070275
A;Accession: JC5368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dynactin 1 - mouse
N;Alternate names: p150 Glued
C;Species: Mus musculus (house mouse)
C;Date: 28-May_1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
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R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
Nucleic Acids Res. 29, 2145-2153, 2001
A;Tille: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: F90577
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A;Residues: 1-1281 <JAN
A;Cross-references: UNIPROT:008788; GB:U60312; NID:g2104494; PIDN:AAB57773.1; PID:g21044
A;Bxsperimental source: brain
C;Comment: This protein is a member of the oligomeric dynactin complex that is required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;Nolecule type: DNA
.;Residues: 1-314 <KUR>
.;Residues: 1-314 <KUR>
.;Cross-references: UNIPROT:Q98Q43; GB:AL445566; PID:gl4089940; PIDN:CAC13699.1; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lipoprotein vsaE [imported] - Mycoplasma pulmonis (strain UAB CTIP) (fragment);Species: Mycoplasma pulmonis
;Species: Mycoplasma pulmonis
;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Gene: MYPU 5260
;Genetic code: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession:
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Best Local Similarity 36.6
Matches 15; Conservative
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                            Gene: Dctn1
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                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 ITEEQKAKFKDVIQDARTKLQDLTTKLEKIKS--EKENIEKKLDPII 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VKETPQQKYQRLLHB----VQBLTTEVEKIKTTVKESATEEKLTPVL 44
                                                                                                                                                                                                         4 ETPOOKYORLLHEVOELTTEVEKIKTTVKESATEEKLTPVLLAKOL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GVKE-TPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKL 40
                                                                                                                                                                                                                                                         h 24.9%; Score 62.5; DB 2; Length 1281; Similarity 34.8%; Pred. No. 1.8e+02; 16; Conservative 11; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                          Caenorhabditis elegans
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T32222 R;Davidson, S.; Wohldmann, P.; Gillam, B. submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid T23B12. A;Reference number: Z21137 A;Accession: T32222 A;Accession: T32222 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                         A;Gene: CESP:T23B12.7
A;Map position: 5
A;Introns: 67/3
                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:017002; EMBL:AF022982; PIDN:AAB69938.1; GSPDB:GN00023; CESP:A;Experimental source: strain Bristol N2; clone T23B12
C;Genetics:
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                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-296 < DAV>
                                                                                     Matches
                                                                                                        Query Match
Best Local Similarity
132 KKTDQRNFK---EEIEAIRRQLEKEVNEEVKQKATLMKTEREKHQKSQEKLTPRLLLK 186
                                                                                     18;
                                         3 KETPOOKYORLLHEVOELTTEVEK-IKTTVKESAT-----
                                                                                     Conservative
                                                                                                        24.7%;
                                                                                   12; Mismatches
                                                                                                      Score 62; DB
Pred. No. 40;
                                                                                                                               2
                                                                                     12;
                                                                                                                               Length 296;
                                                                                     Indels
                                         -----EEKLTPVLLAK 47
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Search completed: November 3, 2005, 22:04:16 Job time : 18.9091 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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47.5
47.5
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48.5
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Match
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1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgm2_6/ptodata/1/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               November 3, 2005, 21:51:39; Search time 15.4011 Seconds (without alignments)
145.410 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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138
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
           DB
                             US-09-270-767-36154
US-09-637-145-2
US-09-637-145-2
US-09-621-976-4332
US-09-107-532A-6433
US-09-107-532A-6433
US-09-513-99C-6026
US-09-513-99C-6026
US-09-107-532A-6432
US-09-644-827B-8
US-09-644-827B-8
US-09-644-827B-7
US-09-644-827B-7
US-09-644-827B-1198
US-09-644-827B-7
US-09-644-827B-7
US-09-166-350-13
US-09-272-419-2
US-09-732-210-1198
US-09-732-210-1198
US-09-286-981B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513545
Sequence 36154, A Sequence 2, Appli A Sequence 2, Appli Sequence 4332, Ap Sequence 6675, Ap Sequence 6026, Ap Sequence 6133, Ap Sequence 6132, Ap Sequence 6432, Ap Sequence 6432, Appli Sequence 11, Appli Sequence 13, Appli Sequence 11, Appli Sequence 1198, Ap Sequence 1198, Ap Sequence 2, Appli Sequence 11, Appli Sequence 14, Appli Sequence 14, Appli Sequence 11, Appli Sequence 256, Appli Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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Query Match Best Local Similarity 40.0%; Pred. No. 7.6 Matches 14; Conservative 6; Mismatches	RESULT 2 US-09-270-767-51371 ; Sequence 51371, Application US/09270767 ; Patent No. 6703491 ; GENERAL INFORMATION: ; APPLICANT: Homburger et al. ; TITLE OF INVENTION: Nucleic acids and proteins ; FILE REFERENCE: File Reference: 7326-094 ; CURRENT APPLICATION NUMBER: US/09/270,767 ; CURRENT FILING DATE: 1999-03-17 ; NUMBER OF SEQ ID NOS: 62517 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 51371 ; EBGOTH: 136 ; TYPE: PRT ; ORGANISM: Drosophila melanogaster US-09-270-767-51371	Query Match 37.0%; Score 51; DB 4 Best Local Similarity 40.0%; Pred. No. 7.6; Matches 14; Conservative 6; Misatches Qy 2 VEKIKTTVKESATEBKLTPVLLAKQLAAL :: : :: : : : : Db 37 IDKVKTTPTANPKTKPTSNNMKLSAVLLAIALLAL	RESULT 1 US-09-270-767-36154 ; Sequence 36154, Application US/09270767 ; Patent No. 6703491 ; GENERAL INFORMATION: APPLICANT: Homburger et al. TITLE OF INVENTION: Nucleic acids and prote; FILE REFERENCE: File Reference: 7326-094 ; CURRENT APPLICATION NUMBER: US/09/270,767 ; NUMBER OF SEQ ID NOS: 62517 ; NUMBER OF SEQ ID NOS: 62517 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 36154 LENGTH: 136 ; TYPE: PRT ; ORGANISM: Drosophila melanogaster US-09-270-767-36154	ALIGNMENTS	28 47 34.1 940 4 US-09-328-352-8165 29 47 34.1 962 4 US-09-071-035-246 30 47 34.1 962 4 US-09-071-035-250 31 47 34.1 962 4 US-09-071-035-250 32 47 34.1 962 4 US-09-071-035-470 33 47 34.1 962 4 US-09-071-035-470 34 47 34.1 962 4 US-09-071-035-474 34 47 34.1 962 4 US-09-071-035-474 35 47 34.1 962 4 US-09-071-035-478 36 46.5 33.7 1964 3 US-09-134-000C-569 37 46 33.3 192 4 US-09-248-7967-206 38 46 33.3 356 4 US-09-248-7967-206 49 46 33.3 757 3 US-09-312-157-6 40 46 33.3 757 3 US-09-312-157-6 41 46 33.3 1595 4 US-09-312-157-6 42 46 33.3 1896 4 US-09-312-157-6 43 45 32.6 85 4 US-09-32-210-1119 44 45 32.6 113 4 US-09-286-981B-1
DB 4; Length 136; 7.6; nes 9; Indels 6; Gaps 1;	eins of Drosophila melanogaster	DB 4; Length 136; 7.6; 9; Indels 6; Gaps 1; 2LAAL 30 NLLAL 71	reins of Drosophila melanogaster	IS .	52-8165 Sequence 8165, Ap 55-246 Sequence 246, App 35-250 Sequence 250, App 35-254 Sequence 254, App 35-470 Sequence 470, App 35-474 Sequence 474, App 35-478 Sequence 478, App 35-478 Sequence 478, App 00C-5691 Sequence 5691, Ap 7-1 Sequence 1, Appli Ap 77-1 Sequence 20678, A DOC-4956 Sequence 6, Appli Sequence 10119, Ap 10-1119 Sequence 11119, Ap 10-1119 Sequence 1, Appli Sequence 1, Appli

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2 VEKIKTT-----VKESATEEKLTPVLLAKQLAAL 30

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APPLICANT: EVANS, RONALD M.
APPLICANT: KAO, HUNG-YING
APPLICANT: KAO, HUNG-YING
APPLICANT: ORNONES, MICHAEL
APPLICANT: ORDENTLICH, PETER
TITLE OF INVENTION: NOVEL HISTONE DEACETYLASE, ANI
FILE REFERENCE: SALK3000
CURRENT APPLICATION NUMBER: US/09/637,145
CURRENT APPLICATION NUMBER: 2000-08-11
NUMBER OF SEQ ID NOS: 4
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                 RESULT 5
US-09-107-532A-6433
; Sequence 6433, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
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                                                                                                                                                                          S
                                                                                                                                                                                                                                                                          ; FEATURE:
, NAME/KEY: UNSURE
; LOCATION: 66
; OTHER INFORMATION: Xaa =
US-09-621-976-4332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-621-976-4332
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US-09-637-145-2
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TYPE: PRT
ORGANISM: Mus sp.
US-09-637-145-2
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patent.pm
SEQ ID NO 4332
LENGTH: 119
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09637145 Patent No. 6673587 GENERAL INFORMATION:
                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local S
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
APPLICANT: Lynn A Doucette-Stamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 RSAVASSVVKQKLAEVILKKQQAAL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4332, Application US/09621976
5. 6639063
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                                                                                                                                           62 ELDKXKTTMKSSVQEECVSTISSSKDEDPLAA 93
                                                                                                                                                                 1 EVEKIKTTVKESATEEKLTPVLLAKQ---LAA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Conservative
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Similarity 44.0%;
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                                                                                                                                                                                                                        35.9%;
                                                                                                                                                                                                          Score 49.5; DI
Pred. No. 11;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB
Pred. No. 94;
   and David Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 938,
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    NAME/KEY: misc_feature
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    LOCATION: (B) LOCATION 1...413
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SEQUENCE DESCRIPTION: SEQ ID NO: 643
US-09-107-532A-6433
                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-09-107-532A-6675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                  Sequence 6675, Application US/09107532A Patent No. 6583275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 6433:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: <Unknown>
COPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ALINI-1010, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERRENCES/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                NUMBER OF SEQUENCES: 7310 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 413 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RC
                                                                                                                                                                                                                                                              APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEB: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 EIERSQTAVVELTKENRLTPGGVVLTK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVEKIKTTVKESATEEKLTP--VLLAK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                  STATE: Massachusetts
                                                                                                                                   CITY: Waltham
                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                          100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD/ROM ISO9660
                                    CD/ROM IS09660
                                                                                                                                                                                                                                           ENTEROCOCCUS
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Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                        and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 413;
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NAME/KEY: misc feature;
LOCATION: (B) LOCATION 1...1027;
SEQUENCE DESCRIPTION: SEQ ID NO: 6675;
US-09-107-532A-6675
 S
                                                                                                           ; OTHER INFORMATION: Xaa=Gln or Arg US-09-513-999C-6026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-513-999C-6026
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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59 US2 REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6783961
GENERAL INFORMATION:
                                      Matches
                                                                                                                                                                                                                                                     SEQ ID NO 6026
                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                            FEATURE:
NAME/KEY: UNSURE
LOCATION: 46
                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6675: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: U$/09/107,532A

PILING DATE: 30-Um1-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              788 EIERSQTAVVELTKENRLTPGGVVLTK 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6026, Application US/09513999C
                                      11;
                                                                                                                                                                                                                                      124
1 EVEKIKTTVKESATE-EKLTPVLLAKQL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVEKIKTTVKESATEEKLTP--VLLAK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1027 amino acids
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.5%;
                                  35.1%; Score 48.5; I
39.3%; Pred. No. 15;
Live 10; Mismatches
                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 4;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                     4;
                                  6
                                                                     Length 124;
                                    Indels
                                  1;
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                                  Gaps
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                                  1;
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; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-470-512A-14
                                                                                                                                                                               RESULT 10
US-09-107-532A-6432
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                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-45139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-270-767-45139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
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                                                                 Sequence 6432, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SOFTWARE: PatentIn Ver. 2.0
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Patent No. 6376652
GENERAL INFORMATION:
APPLICANT: PhageTech, Inc.
TITLE OF INVENTION: Compositions and methods involving a TITLE OF INVENTION: Gene and its encoded protein FILE REFERENCE: 21715/1000
CURRENT APPLICATION NUMBER: US/09/470,512A
CURRENT FILING DATE: 1999-12-12
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 451
TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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               NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 VRELKUSLODOTLEEKLNMVKTTPVLMLDDIGA 203
                                                                                                                                                                                                                                                        79 EEEKVKRSLKQAAQKNDRDTCVILAKEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 EEEKVKXSVKDAAKKGQKDVCIVLAKEM
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STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                 35.1%;
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33.3%;
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Pred. No. 67;
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Pred. No. 3
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                                                                   and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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CITY: Waltham STATE: Massachusetts COUNTRY: USA

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                                        ; LENGTH: 1200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-644-827B-8
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  Query Match
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                                                                                                                             SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 8
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                                                                                                                                                                                                                               APPLICANT: WALLACH, David
APPLICANT: SCHUCHMANN, Marcus
APPLICANT: GONCHAROV, Tanya
TITLE OF INVENTION: Caspase-8 Interacting Proteins
FILE REFERENCE: WALLACH-26
CURRENT APPLICATION NUMBER: US/09/644,827B
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 132105
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                     PRIOR APPLICATION NUMBER: 127721
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 10
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INFORMATION FOR SEQ ID NO: 6432:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: ULLY 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ATTICL NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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LOCATION: (B) LOCATION 1...107
SEQUENCE DESCRIPTION: SEQ ID NO: 6432:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 34.8%; Score 48; DB 4; Length 107; Similarity 47.6%; Pred. No. 15; 10; Conservative 4; Mismatches 7; Indels
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OPERATING SYSTEM: <Unknown>
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  34.8%; Score 48;
  DB 4;
Length 1200;
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APPLICANT: WALLACH, David
APPLICANT: SCHUCHMANN, Marcus
APPLICANT: SCHUCHMANN, Tanya
APPLICANT: GONCHAROV, Tanya
TITLE OF INVENTION: Caspase-8 Interacting Proteins
FILE REFERENCE: WALLACH=26
CURRENT APPLICATION NUMBER: US/09/644,827B
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 132105
PRIOR APPLICATION NUMBER: 132721
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                       ; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-350-13
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US-09-166-350-13
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SOFTWARE: FRSESEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 167
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Patent No. 6762283
GENERAL INFORMATION:
                                               Best Local Similarity 40.6%; Matches 13; Conservative
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Best Local Similarity 42.3%;
Matches 11; Conservative
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Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew
APPLICANT: Chen, Yao
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd
APPLICANT: Old, Lloyd
APPLICANT: Mager, Elke
APPLICANT: Knuth, Alex
TITLE OF INVENTION: Renal Cancer Associated Antigens and
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: L0461/7051
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/166,350A
CURRENT FILING DATE: 1998.10-05
EARLIER APPLICATION NUMBER: US 09/166,350
EARLIER FILING DATE: 1998-10-05
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 VACAVASSVVKQKLAEVILKKQQAAL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 VACAVASSVVKQKLAEVILKKQQAAL 173
1 EVEKIKTTVKESATEEKLTPVLLAKQ---LAA 29 | |::| |||:| | | | ::: : :| |||
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                                                           7; Mismatches
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4; Mismatches 11
                                                                                Score 47.5;
Pred. No. 30;
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Pred. No. 2.9e+02;
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                                                                                                  DB 4;
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Search completed: November 3, 2005, .22:05:55 Job time : 16.4011 secs
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 1756951CD1
US-09-976-594-421
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US-09-976-594-421
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; ORGANISM: Myxococcus xanthus
US-09-902-540-16180
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US-09-902-540-16180
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Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SOFTWARE: PERL Program
SEQ ID NO 421
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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 16180
LENGTH: 314
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 Matches
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 388-10(15849)B
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                                                                                                                                                                                   62 ELDKWKTTMKSSVQEECVSTISSSKDEDPLAA 93
                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                  1 EVEKIKTTVKESATEEKLTPVLLAKQ---LAA 29
                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       34.4%;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

21: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

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26: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

27: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

28: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1867879 seqs, 418409474 residues
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Gapop 10.0 , Gapext 0.5
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138
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10 11	4 10 0 1	ω 2 μ	Result No.
133 103 56 51	138 135 135	138 138 138	Score
96.4 74.6 40.6 37.0	100.0 100.0 97.8 97.8	100.0	Query Match Length DB
52 23 334 447	465 465 183 224	134 401 406	Length
10 18 15	9 14 10	14 16	₽B
US-09-782-816A-51 US-09-782-816A-1 US-10-501-282-4734 US-10-335-977-7239	US-09-925-298-676 US-10-102-806-676 US-09-782-816A-54 US-10-425-115-315831	US-10-106-698-6730 US-10-408-765A-1369 US-09-782-816A-53	ID
Sequence 51, Appl Sequence 1, Appli Sequence 4734, Ap Sequence 7239, Ap	Sequence 676, App Sequence 676, App Sequence 54, Appl Sequence 315831,	Sequence 6730, Ap Sequence 1369, Ap Sequence 53, Appl	Description

ALIGNMENTS

Qy . 1 EVEKIKTTVKESATBEKLTPVLLAKQLAAL 30	Query Match 100.0%; Score 138; DB 14; Length 134; Best Local Similarity 100.0%; Pred. No. 2.3e-11; Matches 30; Conservative 0; Mismatches 0; Indels 0; G	; FEATURE; ; NAME/KEY: MISC FEATURE ; LOCATION: (126) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-6730	; SEQ 10 NO 5/30 ; LENGTH: 134 ; TYPE: PRT ; ORGANISM: Homo sapiens	; PRIOR FILING DATE: 1999-11-03 ; NUMBER OF SEQ ID NOS: 8564 ; SOFTWARE: Patentin Ver. 3.0	PRIOR APPLICATION NUMBER: US 60/163,280 PRIOR FILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: US 60/157,137 PRIOR APPLICATION NUMBER: US 60/157,280	; GENERAL INFORMATION: ; APPLICANT: Ruben et al. ; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide ; FILE REFERENCE: PA005P1 ; CURRENT APPLICATION NUMBER: US/10/106,698	RESULT 1 US-10-106-698-6730 Sequence 6730, Application US/10106698 ; Publication No. US20030109690A1
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EVEKIKTTVKESATEEKLTPVLLAKQLAAL

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SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 406
TYPE: PRT
ORGANISM: Homo sapiens
US-09-782-816A-53
                US-09-925-298-676
Sequence 676, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1369
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                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PROTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPBUTIC INTERVENTION
TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION UNMERER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTMARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1369
                                                                                                                                                                                                                 Query Match
Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1369, Application US/10408765A Publication No. US20040101874A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53, Application US/09782816A Publication No. US20030032771A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ghosh, Soumicra
APPLICANT: Fahy, Boin D.
APPLICANT: Rosen et al
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: UC069.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 EVEKIKTTVKESATEEKLTPVLLAKQLAAL 145
                                                                                                                                          121 EVEKIKTTVKESATEEKLTPVLLAKQLAAL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVEKIKTTVKESATEEKLTPVLLAKQLAAL 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang, Bing
                                                                                                                                                                                                             100.0%; Score 138; DB 10; llarity 100.0%; Pred. No. 8.5e-11; Conservative 0; Mismatches 0;
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Pred. No. 8.4e-11;
Mismatches 0;
                                                                                                                                                                                                                                               Length 406;
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; OTHER INFORMATION: Xaa
US-10-102-806-676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 676
LENGTH: 465
                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                 NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: 1
NAME/KEY: SITE
LOCATION: (16)
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCATION: (6)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (16)
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NAME/KEY: SITE
                                                                                                                                  LOCATION: (5)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                   NAME/KEY: SITE
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                 any of the naturally
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Pred. No. 1e-10;
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                 occurring L-amino acids
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                                                                          L-amino acids
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Query Match 100.0%; Score 138; DB 1
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 30; Conservative 0; Mismatches

DB 14;

Length 465;

Indels

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Gaps

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RESULT 8
US-09-782-816A-51
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US-10-425-115-315831
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                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: MRT4577_51109C.1.pep US-10-425-115-315831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 54, Application No. US20
GENERAL INFORMATION
Sequence 51, Application US/09782816A Publication No. US20030032771A1
                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 315831
LENGTH: 224
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: F
SEQ ID NO 54
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 315831, Application US/10425115 Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 EVEKIKTTVKESATEEKLTPVVLAKQLAAL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVEKIKTTVKESATEEKLTPVLLAKQLAAL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 4.0
                                                                                                           EVEKIKTTVKESATEEKLTPVVLAKQLAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVEKIKTTVKESATEEKLTPVLLAKQLAAL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09782816A
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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96.7%;
                                                                                                                                                                                                97.8%;
96.7%;
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Pred. No. 8.7e-11;
1; Mismatches (
                                                                                                                                                                            Score 135; DB 16;
Pred. No. 1.1e-10;
1; Mismatches C
                                                                                                           98
                                                                                                                                                                                                                  DB 16;
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                                                                                                                                                                                                              Length 224;
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RESULT 10 US-10-501-282-4734

Sequence 4734, Application US/10501282 Publication No. US20050203280A1 GENERAL INFORMATION:

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                                                                                                                                   US-09-782-816A-1
                                                                                                                                                                                                                                                                                                    SOFINAL SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENCTH: 52
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09782816A Publication No. US20030032771A1
                                                                 Matches
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: UC069.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: UC069.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa = Val or Leu OTHER INFORMATION: A sequence conserved OTHER INFORMATION: musculus.
                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                     NAME/KEY: UNSURE LOCATION: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                                     ORGANISM: Unknown
                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 44
                                                                                 Local
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                                                                                                                                                   INFORMATION:
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                                                                Similarity 95.7
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVEKIKTTVKESATEEKLTPVLLAKQLAAL 30
                     EVEKIKTTVKESATEEKLTPVLL 23
EVEKIKTTVKESATEEKLTPVXL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rogers, Gregory C.
                                                                                                                                                  Xaa = Val or Leu
The sequence is a Homo sapiens sequence when Xaa
represents Leu and a Mus musculus sequence when
Xaa represents Val.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.4%;
96.7%;
                                                                                74.6%;
95.7%;
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                                                                Score 103; DB 10;
Pred. No. 2.3e-07;
0; Mismatches 1;
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Pred. No. 3.8e-11;
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TITLE OF INVENTION: ALLOICOCCUS OTITIDIS OPEN READING PRA
TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COM
FILE REFERENCE: AM100780 L2
CURRENT APPLICATION NUMBER: US/10/501,282
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: 60/333,777
PRIOR FILING DATE: 2001-11-29
PRIOR PRIOR APPLICATION NUMBER: 60/426,742
PRIOR APPLICATION NUMBER: FCT/US02/36123
PRIOR FILING DATE: 2002-11-18
PRIOR FILING DATE: 2002-11-25
PRIOR FILING DATE: 2002-11-25
PRIOR FILING DATE: 2002-11-25
PRIOR FILING DATE: 2002-11-25
NUMBER: OF SEQ ID NOS: 6653
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US-10-335-977-7239
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TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-4734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7239, Application US/10335977

Publication No. US20040052799A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLERIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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                                                                                                                         INFORMATION FOR SEQ ID NO: 7239: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            PILING DATE: 30-Dec-2002

PRIOR APPLICATION NUMBER: 08/993,002

APPLICATION NUMBER: 08/993,002

PILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 35,207

REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (611)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                     TOPOLOGY: linear MOLECULE TYPE: protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 IDQIKSTIKSGSVKTKLGGLLIKKDLSSL 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: Massachusetts
                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 28 State Street
                                                                                                                                                                            TELEFAX: (617)742-4214
                                                                                                 LENGTH: 447 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD
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RUSSELL, DAVID PARRISH
FLETCHER, LEAH DIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02109-1875
YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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LOCATION: (B) LOCATION 1...447
SEQUENCE DESCRIPTION: SEQ ID NO: 7239:
US-10-335-977-7239
                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...773
SEQUENCE DESCRIPTION: SEQ ID NO: 7240:
US-10-335-977-7240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-10-335-977-7240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7240, Application US/10335977

publication No. US20040052799A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                  Matches
                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7240:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: Windows NT 4.0
SOPTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
                                                                                     Local Similarity
                                                                                                                                                                                                                                                                  MOLECULE TYPE: pro
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 LKQFVKDSAKKELLTPIIAFKSM 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
5 IKTTVKESATEEKLTPVLLAKQL 27 :| ||:|| :| ||:: | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 IKTTVKESATEEKLTPVLLAKQL 27
                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                 ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 State Street
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43.5%;
                                                                                 37.0%;
                                                                                                                                                                                                                                                                                                             protein
                                                             Score 51; DB 15; L
pred. No. 2.8e+02;
pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
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Pred. No. 1.5e+02;
                                                                                                        Length 773;
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                                                                  Indels
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                                                                  Gaps
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222 LKQFVKDSAKKELLTPIIAFKSM 244

US-10-282-122A-47253

RESULT 13

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RESULT 14
US-10-732-923-20606
; Sequence 20606, Application US/10732923
; Publication No. US20050108791A1
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SEQ ID NO 47253
LENGTH: 932
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Publication No. US20040029129A1
             APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                          10-282-122A-47253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITEA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
APPLICATION NUMBER: 10/310,154
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APPLICATION NUMBER: 60/253,625
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Zyskind, Judith
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Carr, Grant
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Malone, Cheryl
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Pred. No. 3.5e+02;
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Search completed: November Job time: 56.0642 secs
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                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: MRT4577_125287C.1.pep US-10-425-115-212374
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US-10-425-115-212374
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                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 212374
LENGTH: 211
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NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 20606
LENGTH: 10917
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Best Local Similarity 46.2%;
Matches 12; Conservative
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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                                                            2105692 seqs, 386760381 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Aau36796 Staphyloc	Aau34139 Staphyloc	В	Abb65359 Drosophil	Abp52976 Cellular		Abb59088 Drosophil	7	S		ω			σ	0	_	œ	Aag75956 Human col	Cellul	Mouse p	Breast	8 Human	Adj69563 Human hea	Abp98851 Human str	Abm81421 Tumour-as	tion	_

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and

New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

N-PSDB; ACN39497. WPI; 2004-347921/32. Wu ID,

Zhou ۲, (GETH)

GENENTECH INC. Zhang Z,

02-OCT-2002; 2002US-0414971P.

Claim 12; SEQ ID NO 3675; 7273pp; English.

. 45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
64	64	64	64	64	64	64	65.5	65.5	66	66	66	66	67	67	67	67	67	67	67
25.5	25.5	25.5	25.5	25.5	25.5	25.5	26.1	26.1	26.3	26.3	26.3	26.3	26.7	26.7	26.7	26.7	26.7	26.7	26.7
188	188	188	188	188	151	140	1837	207	1020	868	386	13	2481	2481	2478	2478	2478	2478	1448
σ	σ	4	ω	N	w	4	œ	4	4	N	σ	σ	7	σ	σ	σ	4	4	6
ABU80870	AB017616	AAU12172	AAB10278	AAW64545	AAG03725	AA012168	ADS44304	AAB29754	AAM79875	AAY37731	ABU44043	ABP52977	ABR62804	ABU15838	ABM71899	ABJ19002	AAU34320	AAU37374	ADA89551
Abu80870	Abo17616	Aau12172	Aab10278	Aaw64545	Aag03725	Aao12168	Ads44304	Aab29754	Aam79875	Aay37731	Abu44043	Abp52977	Abr62804	Abu15838	Abm71899	Abj19002	Aau34320	Aau37374	Ada89551
Human PRO	Novel hum	Human PRO	Human fet	Human sto	Human sec	Human pol	Bacterial	Rice PNI-	Human pro	Protein i	Protein e	Cellular	Methicill	Protein e	Staphyloc	Pathogen	Staphyloc	Staphyloc	Staphyloc

ALIGNMENTS

RESULT 1 ABM81421 tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; 29-SEP-2003; 2003WO-US028547. 15-APR-2004. WO2004030615-A2 Homo sapiens. gene therapy; cytostatic. Tumour-associated antigenic target; TAT; human; overexpression; Tumour-associated antigenic target (TAT) polypeptide PRO82191, SEQ:3675. 18-NOV-2004 ABM81421; ABM81421 standard; protein; 314 (first entry) B

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RRESULT 2
ABP98817
IID ABP9
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Best Local
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02-NOV-2001;
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                                                                                                                                                                                      Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; antianginal; neuroprotective; cerebroprotective; hypotensive; cardiant; osteopathic; antiinflammatory; antiarthritic; virucide; gene therapy; human; stroke; structural and cytoskeleton-associated protein; SCAP; cancer; angina;
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07-DEC-2001;
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human structural and diagnosing, treating
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Elliott VS,
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; 2001US-0343896P.
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cytoskeleton-associated and preventing diseases
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Pred. No. 6e-21;
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                                                                                                                                                                                                                                                                                                            11 JD, Chang H;
Gorvad AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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proteins (SCAP) useful or conditions associat

Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating the state of the sample and correlating the sample and cor

correlating

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ARBSULT 3
ADJ69563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a novel isolated human structural and CC cytoskeleton-associated protein (SCAP) polypoptide. The polypoptides and CC polynucleotides encoding them are useful in diagnosing, treating and CC preventing diseases or conditions associated with the decreased CC expression or over expression of SCAP, such as cell proliferative (e.g. Cc cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's CC cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's CC disease, stroke), heart (e.g. hypertension, heart failure, angina) and consecutions. These are also useful in assessing the effects of exogenous CC infections. These are also useful in assessing the effects of exogenous CC compounds on the expression of nucleic acid and amino acid sequences of CC SCAP. The SCAP or its fragments are useful in screening compounds for CC effectiveness as agonist or antagonist of the polypeptides, or in CC altering the expression of the target polymolectian and compounds that Specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein protein profiles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                        12-APR-2002;
17-JUN-2002;
20-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-2004
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                                                                                                                          WPI; 2003-845369/78
                                                                                                                                                                                       Ghosh SS,
Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-APR-2003; 2003WO-US010870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteopathic; ophthalmological; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human heat mitochondrial protein as a therapeutic target SeqID1369.
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                                                                                                                                                                                                                                                                                                              (-OTIM)
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52; Conserv
                                                                                                                                                                                                                                                                              BUCK INST
                                                                                                                                                                                                                                                                                                              MITOKOR
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                                                                                                                                                                                                                 Fahy ED,
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2002US-0389987P.
2002US-0412418P.
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                                                                                                                                                                                                                                                                                 AGE
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Pred. No. 7.4e-21;
                                                                                                                                                                                                                    Gibson BW,
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Claim 1;

SEQ ID NO 1369; 180pp; English

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERAF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; psi inhibitor; leukaemia; lymphoid malignancy; neuronal disorder; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder;
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                                                                                   Disclosure; Fig 1; 55pp; English
                                                                                                                                                                      New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-657599/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sharp DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rogers GC,
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llarity 100.0%;
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Pred. No. 7.9e-21;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulgant antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
                           Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are
                                                                                                                         Claim 11; Page 1126-1128; 1299pp;
                                                                                                                                                                                                                     New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF21871
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-611515/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disorder; wound healing; neurological disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB58968 standard; protein; 465
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                                                                                                                                                                                             neurological diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovarian cancer associated antigen protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 8.1e-21
; Mismatches (
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                                                                                                                             English.
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antifungal; antiparastic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune themolytic anaemia, autoimmune thyroiditis, diabetes multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular diseases such as myocardial ischaemias, wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; p50 inhibitor; leukaemia; lymphotid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
                                                                                                                                                New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are sequences given in ABP52966 and ABP52967 and can have C-terminal and I terminal extensions. (I) have cytostatic and antiinflammatory activities.
                                                                                                                                                                                                                                                                                                      (REGC )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse p50 amino acid sequence SEQ ID NO:54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infectious diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunologic disorder.
                                                                                                                                                                                                                              2002-657599/70
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                                                                                                                                                                                                                                                               Rogers GC,
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Pred. No. 9.4e-21;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellular proliferation inhibition; cytostatic; antiinflammatory; cancer; p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory; glandular disorder; macrophagal disorder; epithelial disorder; stromal disorder; blastocoelic disorder; angiogenic disorder;
                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
Synthetic.
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                                                                                                                     immunologic disorders.
                                                                                                                                          New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2001; 2001US-00782816
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Pred. No. 7.1e-21;
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Best Local S
Matches 51
AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders; and inflammatory, angiogenic and immunologic disorders. The present sequence represents a specifically claimed peptide inhibitor of cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen
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03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-2000; 2000WO-US026524.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acids encoding 4277 human colon cancer-associated polypeptides, for preventing, diagnosing and/or treating colorectal cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVXLAKQLAAL
                                                                                                                                                                                                                                                                                                                                                                                                                              Page 8181; 9803pp; English.
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98.1%;
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Pred. No. 2.8e-21;
0; Mismatches 1
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                           The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to produce the colon cancer-associated Ps, by inserting the nucleic acid into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP52968
                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 29; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide inhibitors of p50/dynamitin useful for treating cancinhibiting cellular proliferation, e.g. benign or malignant tumcleukemia and lymphoid malignancies, or inflammatory, angrogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-657599/70.
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stromal disorder; blastocoelic disorder;
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glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
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[larity 100.0%; Pred. No. 4.8e-19;
Conservative 0; Mismatches 0;
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                           The present invention describes an isolated peptide (I) comprising or having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disporders such as neuronal, glial, astrocytal, hypothalamic and other glandular,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and immunologic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
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                  The present invention describes an isolated peptide (I) comprising or CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-CC terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The CC peptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such CC as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC thyroid, hepatic carcinomas, sarcomas, glioblatomas, and various head and CC neck tumours); leukaemias and lymphoid malignancies, other disorders such CC as neuronal, glial, astrocytal, hypothalamic and other glandular, as neuronal, glial, astrocytal, hypothalamic and other glandular, CC inflammatory, angiogenic and immunologic disorders. The present sequence cropresents a peptide that can be N-terminally added to (P1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide inhibitors of p50/dynamitin useful for treating cancer inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
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Pred. No.
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The present invention describes an isolated peptide (I) comprising or the ving at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antinflammatory activities can dean be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention care useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, cas benign or malignant tumours (renal, liver, kidney, bladder, breast, cas benign or malignant seconds, glioblatomas, and various head and carcinomas, such carcinomas, such as neuronal, pleukaemias and lymphoid malignancies, other disorders such neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, can macrophagal, epithelial, stromal and blastocoelic disorders; and confilammatory, angiogenic and immunologic disorders
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                                                                                                                                                                                                                                                                                                                                         New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p50 inhibitor; dynamitin inhibitor; gene therapy; tumour; carcinoma; sarcoma; glioblatoma; leukaemia; lymphoid malignancy; neuronal disorder; glial disorder; astrocytal disorder; hypothalamic disorder; inflammatory glandular disorder; macrophagal disorder; epithelial disorder;
                                                                                                                                                                                                                                                                                     Claim 1; Page 29; 55pp; English
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                                                                                                                                                                                                                                                                                                                          ımmunologic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stromal disorder; blastocoelic disorder; angiogenic disorder;
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/note= "Leu in humans and Val in Mus musculus"
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CC The present invention describes an isolated peptide (I) comprising or CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-CC terminal extensions. (I) have cytostatic and antiinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The CC apeptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC thyroid, hepatric carcinomas, sarcomas, glioblatomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, CC macrophagal, epithelial, stromal and blastocoelic disorders; and confidential, stromal and blastocoelic disorders; and confidential approaches appeared that can be N-terminally added to (P1)
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95.7%;
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Pred. No. 5.3e-05;
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Sequence 19

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Query Match

Length 19;

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CC dastric, ovarian, colorectal, prootate, pancreatic, lung, vulval, compastic, verminal astroxytal, hypothalamic and various head and considers such compassa, epithelial, stromal and happothalamic considers such confideration, astroxytal, stromal and blastocoelic disorders, and confideration, such confideration, such confideration, such confideration, converted, prostate, pancreation, lung, vulval, confideration, such confideration, such confideration, such confideration, such confideration, converted, prostate, pancreatic, lung, vulval, confideration, such confideration, such confideration, such confideration, such confideration, confideration, such confideration, confideration, such confideration, confideration, such confideration, confideration, confideration, confideration, confideration, confideration, confideration, confideration, confideration, stromal and blastocoelic disorders, and confideration, applied that can be N-terminally added to (P1)
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Matches 18
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glandlal disorder; astrocytal disorder; hypothalamic disorder; inflammatory;
glandular disorder; macrophagal disorder; epithelial disorder;
stromal disorder; blastocoelic disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide inhibitors of p50/dynamitin useful for treating cancer by inhibiting cellular proliferation, e.g. benign or malignant tumors, leukemia and lymphoid malignancies, or inflammatory, angiogenic and
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                                                                         Sequence 18
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                                                                                                                                                                                                                                                                                                                                                                                                                           immunologic disorders.
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   / Match 37.1%; Score 93; DB Local Similarity 100.0%; Pred. No. 0. nes 18; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                   present invention describes an isolated peptide (I) comprising or ing at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
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DB 5; Le...
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                                                          The present invention describes an isolated peptide (I) comprising or CC having at least 90% identity to (P1) or (P2). Where (P1) and (P2) are the CC sequences given in ABP52966 and ABP52967 and can have C-terminal and N-terminal extensions. (I) have cytostatic and antinflammatory activities and can be used as p50/dynamitin inhibitors and in gene therapy. The peptides, nucleic acid molecules and methods from the present invention CC are useful for treating cancer by inhibiting cellular proliferation, such as benign or malignant tumours (renal, liver, kidney, bladder, breast, CC gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, CC thyroid, hepatic carcinomas, sarcomas, glioblateomas, and various head and neck tumours); leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, CC macrophagal, pepthelial, stromal and blastocoelic disorders; and crepresents a peptide that can be N-terminally added to (P1)
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   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunologic disorder.
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       17
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   AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO: 8
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Search completed: November 3, 2005, 21:57:29 Job time: 73.1872 secs

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1 PQQKYQRLLHEVQELTT 17

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OM protein - protein search, using sw model	
otein search,	Copyright (
using sw model	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
	5.1.6 Compugen Ltd.

Run on: November 3, 2005, 21:43:09; Search time 18.9091 Seconds (without alignments) 264.596 Million cell updates/sec

Sequence: Title: Perfect score: 09782816-3-1-22 251 GVKETPQQKYQRLLHEVQEL.....ESATEEKLTPVLLAKQLAAL 52

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

					00::::::::	
De 1		*				
No.		Match	Length	DB	ID	Description
L	69.5	27.7	804	2	T32864	hypothetical prote
N	თ	27.1	1742	N	T49451	prot
ω	67.5	26.9	1325	N	S16129	μ.
4.	67	•	1287	N	T22235	
տ	67	26.7	2481	N	D90011	FmtB protein [impo
0	66	26.3	393	N	T04957	thetical
7	66	26.3	866	N	C71509	
œ	65.5	26.1	1837	N	T41023	nucl
9	9	25.5	210	N	E84499	prot
10	63.5	25.3	163	N	869518	•
11	63.5	25.3	374	N	D70391	
12	63	25.1	281	N	F75216	
13	63	25.1	314	N	F90577	•
14	62.5	24.9	1281	N	JC5368	dynactin 1 - mouse
15	62	24.7	296	N	T32222	ical
16	62	24.7	2469	N	H36812	hypothetical prote
17	61	24.3	442	N	C95070	sensor histidine k
18	61	24.3	442	N	A97938	vncS, histidine ki
19	60.5	24.1	819	N	AC2029	hypothetical prote
20	60.5	24.1	1214	N	JC2069	
21	60	23.9	523	N	S06920	
22	60	23.9	695	N	H72243	~
23	59.5	23.7	279	N	D71453	hypothetical prote
24	9	•	665	N	S62328	õ
25		•	112	N	G72645	prot
26	59	23.5	239	N	D84004	
27		٠	550	N	G85436	
28		•	611	N	E90543	glucose inhibited
29	59	23.5	782	N	A34219	Bic-D protein - fr

RESULT 2 T49451

kinesin-like protein Kif2la related protein [imported] - Neurospora crassa N;Alternate names: protein B14D6.30 C;Species: Neurospora crassa C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004 C;Accession: T49451 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000 A;Reference number: Z25022 A;Accession: T49451

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1742 <SCH>
A;Cross-references: UNIPROT:Q8XOC5; EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.30
A;Experimental source: BAC clone B14D6; strain OR74A

ALIGNMENTS

Ъ	Q	D Qy	Query Ma Best Loo Matches	A;Map p A;Intro C;Super	C; Genetics A; Gene: CE	A;Cross A;Exper	A; Molec A; Resid	A;Acces	A;Descr A;Refer	R;Murra submitt	C:Acces	C;Speci	hypothe	RESULT T32864
426 SAKL 429	49 LAAL 52	2 VKETPOOKYORLLHEVOELTTEVEKIKT-TVKESATEE-KLTPVLLAKO 48 :: : : :	Query Match 27.7%; Score 69.5; DB 2; Length 804; Best Local Similarity 34.4%; Pred. No. 20; Matches 22; Conservative 10; Mismatches 19; Indels 13; Gaps 3;	A;Map position: 1 A;Introns: 52/1; 113/1; 162/3; 201/3; 248/2; 346/1; 433/2; 464/3; 565/3; 628/2; 646/3; 7 C;Superfamily: Caenorhabditis elegans hypothetical protein ZK484.4	C;Genetics: A;Gene: CESP:ZK484.4	A;Cross-references: UNIPROT:Q95X56; EMBL:AF040659; PIDN:AAB95062.1; GSPDB:GN00019; CESP: A;Experimental source: strain Bristol N2; clone ZK484	A; Molecule Lype: DNA A;Residues: 1-804 <mur></mur>	A;Accession: T32864	A;Description: The sequence of C. elegans cosmid ZK484. A;Reference number: Z21237	k;Murray, J.; Wonldmann, P. submitted to the EMBL Data Library, December 1997	C; Accession: T32864	C:)Species: Caenornabditis elegans C:)Species: Caenornabditis elegans	hypothetical protein ZK484.4 - Caenorhabditis elegans	

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A;Status: pt......A;Status: pt...A;Nolecule type: DNA
A;Residues: 1-1287 <WIL>
A;Residues: UNIPROT:062245;
A;Cross-references: UNIPROT:062245;
A;Cross-references: Clone F45G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
$16129
$16129
$16129
Gynein-associated protein, 150K, cytosolic - bovine
Gyspecies: Bos primigenius taurus (cattle)
Gyspecies: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
FmtB protein [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_chan C;Accession: D90011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein R45G2.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004 C;Accession: T22235
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A;Title: Homology of a 150K cytoplasmic dynein-associated polypeptide with the Drosophil A;Reference number: S16129; MUID:91260877; PMID:1828535
A;Accession: S16129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lindsay, S.
submitted to the EMBL Data Library,
A;Reference number: Z19535
A;Accession: T22235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1325 < KKV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Introns: 58/1; 166/1; 267/3; 1543/3
                                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Map position: 6
                                                                                                                                                                                                                                                                                                                                Map position: 3
|Introns: 59/2; 117/3; 153/3; 180/2; 233/2; 341/3; 393/1; 424/2; 551/3; 664/3; 734/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: S16129
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1 Similarity 36.6%;
15; Conservation
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17; Conserv
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                                                                                                                                                                                                                                                               l Similarity
18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAESLQQEVEALKERVDELTTDLEILKAEIEEKGSDGAASSYQL-KQL
                                                                                                                                                                         EPPPEKRQKILEVIDDDFSEFFQEKVKENTKESVAEEKVENSNEELKPPPILRKAVS 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVKETPQQKYQRLLHEVQBLTTEVEKIKTTVKESATEEKLTPVLLAKQL
                                                                                                                                                                                                                    ETPQQKYQRLLHEVQELTTEV--EKIKTTVKESATEEKL-----TPVLLAKQLA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.9%; Score 67.5; Ilarity 34.7%; Pred. No. 56; Conservative 11; Mismatches
                                                                                                                                                                                                                                                               Conservative
                    #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                 26.7%; Score 67;
31.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches
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Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          March 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: Z93382; PIDN: CAB07612.1; GSPDB: GN00021; CESP: F4
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    Query Match
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-2481 <KUR>
A; Cross-references: UNIPROT: Q99QR6;
A; Cross-references: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D90011
                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F7J7.200 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Pate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T04957 C;Accession: T04957 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; submitted to the Protein Sequence Database, July 1998
                                                                                                                                                                                                                                A;Cross-references: UNIPROT:049567; EMBL:AL021960 A;Experimental source: cultivar Columbia; BAC clo C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: C; Genetics:
                                                                                                                                                               A; Map position: 4
A; Introns: 80/1; :
A; Note: F7J7.200
                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-393 <BEV>
                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z15391
A; Accession: T04957
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                                                                                  Matches
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nes 13; Conserv
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  27
                     2 VKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEE 38
QESTQQTHQNLLYKVQ-----KWRTSLKDSSDAELKLSPALV
                                                                                                                                                                                    217/3; 264/1; 291/3
                                                                                Conservative
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35.1%;
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Pred. No.
                                                                                                    Score 66; DB Pred. No. 21;
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                                                                                  Mismatches
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15;
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  63
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K.; I
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A; Gene: pork C; Superfamily: A;Title: Genome sequence of an obligate intracellular pathogen A;Reference number: A71570; MUID:99000809; PMID:9784136 A;Accession: C71509 probable DNA polymerase I - Chlamydia trachomatis (serotype D, strain UW3/Cx) C;Species: Chlamydia trachomatis (c;Species: Chlamydia trachomatis C;Date: 13-Sep_1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004 C;Accession: C71509 A;Cross-references: UNIFROT:O84500; GB:AE001322; GB:AE001273; NID:g3328916; A;Experimental source: serotype D, strain UW-3/Cx A; Residues: 1-866 < ARN> A; Molecule type: DNA A;Status: preliminary R;Stephens, R.S.; Kalman, 1 Science 282, 754-759, 1998 DNA-directed DNA polymerase S.; Lammel, C.J.; Fan, J.; Marathe, æ : of. humans: Chlamydia traci Aravind,

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Mitchell,

PIDN: AAC6809

Score

66;

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2:

Length

866;

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RESULT 10
$69518
hypothetical protein 12 - phage HP1
C;Species: phage HP1
C;Date: 06-Dec-1996 #sequence_revis
C;Accession: S69518
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R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, June 1998
                                                                                                                                                                                                                                                                                                                             A;Map position: 2
C;Superfamily: uncharacterized CYTH domain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-210 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein At2g11890 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 12-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable nuclear pore complex-associated protein - fission yeast (Schizosac C; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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A;Experimental source: strain 972h-; cosmid c162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1837 < MUR>
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A; Accession: T41023
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19; Conserv
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                                                                                                                                                                       GVKLEVDETKYDFGNCYEIECETEEPERVKTMIEEFLTEEKI 191
                                                                                                                                                                                                        GVK-ETPQQKYQ-RLLHEVQELTTEVEKIKTTVKESATEEKL 40
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                 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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Pred. No. 1.3e+02;
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10; Mismatches
                                                                                                                                                                                                                                                                        Score 64; DB 2;
Pred. No. 17;
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                                                                                                                                                                                                                                                                                          Length 210;
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                                                                                                                                          R; anonymous, Genoscope submitted to the EMBL Data Library, July 1999 A; Description: Pyrococcus abyssi genome sequer A; Reference number: A75001 A; Accession: F75216
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D70391
                      A; Experimental source: C; Genetics:
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                                       A;Cross-references: UNIPROT:Q9V217;
A;Experimental source: strain Orsay
                                                                                 A; Residues: 1-281 < KAW>
                                                                                                     A; Molecule type: DNA
                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                             hypothetical protein PAB2181 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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Best Local Similarity
Matches 17; Conser
                                                                                                                                                                                                                                                  Species: Pyrococcus abyssi;Date: 20-Aug-1999 #sequence_revision;Accession: F75216
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19; Conserv
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GB:AJ248283; GB:AL096836; NID:g5457433;

PIDN:CAB4918

20-Aug-1999

#text_change

09-Jul-2004

sequence:

insights

into

archaeal chromosome

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nypothetical protein aq 1060 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: D70391
                                                                                                                                                                           A;Gene: ac_1060
C;Superfamily: multidrug resistance protein A; lipoyl/biotin-binding
                                                                                                                                                                                                                                     A;Residues: 1-374 <AQF>
A;Cross-references: UNIPROT:067159;
A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                              A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: D70391
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A;Title: The complete nucleotide sequence of bacteriophage HP1 DNA.
A;Reference number: S69503; MUID:96279738; PMID:8710508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P51714; EMBL:U24159; NID:g1046235; PIDN:AAB09197.1; PID:g104A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995 C;Superfamily: phage HP1 hypothetical protein 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not A;Molecule type: DNA A;Residues: 1-163 <ESP>
                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Deckert, G.; Warren, P.V.;
164 PRRKFEEVDTNLKVLLHEREYLEKSIQEINTEIKRAKKGI-ENARNEFKTIEELKKELSS
                                           6 PQQKYQR-----LLHE-----VQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAA 51
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                                                                                            Conservative 14;
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                                                                                                             25.3%;
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                                                                                                                  Score 63.5;
Pred. No. 3
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Pred. No. 1
                                                                                                                                                                                                                                                                                    GB:AE000721; NID:g2983544; PIDN:AAC07129.1; PID:g298
                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T.; Young, W.G.;
                                                                                                                     36;
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                                                                                            Gaps
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  222
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RESULT 15
T32222
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F90577
hypothetical protein T23B12.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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A;Cross-references: UNIPROT:Q98Q43; GB:AL445566; PID:g14089940; PIDN:CAC13699.1; GSPDB:
A;Experimental source: strain UAB CTIP
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R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: F90577
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A;Cross-references: UNIPROT:O08788; GB:U60312; NID:g2104494; PIDN:AAB57773.1; PID:g21044
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Jang, W.; Weber, J.S.; Tokito, M.K.; Holzbaur, E.L.F.; Meisler, M.H.
Biochem. Biophys. Res. Commun. 231, 344-347, 1997
A;Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate for the particular of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dynactin 1 - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: JC5368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternate names: p150 Glued
Species: Mus musculus (house mouse)
Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Accession:
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Best Local Similarity 36.6
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         24.9%; Score 62.5; DB 2; 1 Similarity 34.8%; Pred. No. 1.8e+02; 16; Conservative 11: Minnet.
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T32222 R;Davidson, S.; Wohldmann, P.; Gillam, B. submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid T23B12.
A;Reference number: Z21137
                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:017002; EMBL:AF022982; PIDN:AAB69938.1; GSPDB:GN00023; CESP:A;Experimental source: strain Bristol N2; clone T23B12
C;Genetics:
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A; Introns: 67/3
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                                                                                          Conservative
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Search completed: November 3, 2005, 22:04:16
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Listing first 45 summaries
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
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2: uniprot_trembl:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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EMBL; BC009468; AAH09468.1; --
EMBL; BC014083; AAH14083.1; --
EMBL; AY189155; AAO34395.1; --
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the Euro
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI TaxID=10090;
[1]
                                                                                  28-FEB-2003 (Rel. 41, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
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Dynactin complex 50 kDa subunit (50 kDa dynei
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-!- FUNCTION: Modulates cytoplasmic dynein binding to an organ
                                                             Name=Dctn2;
                                                                         23-48K)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0005813; C:centrosome; TAS.
GO:0005869; C:dynactin complex; TAS.
GO:0000776; C:kinetochore; TAS.
GO:0008283; P:cell proliferation; TAS.
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SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
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SUBUNIT: Subunit of dynactin, a multiprotein complex associated
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G.R., Vandekerckhove J.;
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E -> ELE (in Ref. 3).
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Pred. No. 4.
                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                Query Match
                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                              This
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                                                                                               Membrane; Microtubule; Motor INIT_MET 0 0 0 DOMAIN 98 131
                                                                                                                                                  Pfam; PF04912; Dynamitin; 1.
Coiled coil; Cytoskeleton; Direct protein sequencing; Dynein;
                                                                                                                                                                                                                                                                        use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See I
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Subunit of dynactin, a multiprotein complex associated with dynein (By similarity). Interacts with BICD2.
SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.
DEVELOPMENTAL STAGE: Present at high levels in both cytoplasmic and membrane-associated forms in neonates. Levels of membrane-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Modulates cytoplasmic dynein binding to an organelle, and plays a role in prometaphase chromosome alignment and spind organization during mitosis. May play a role in synapse formati during brain development
                                                                                                                                                                                                                                                                                                                                                                                                                                     associated form are greatly reduced in the adult.
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ON, AND
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By similarity.

Coiled coil (Potential).

Coiled coil (Potential).

M; 1535E4ABD5940EBC CRC64;
Score 248;
Pred. No. 9.
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Mismatches

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hotting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schmerch A., Schein J.E.,
RGMCTRAFFIN and intrial analysis of market L. S. Schein J.E.,
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RGMCTRAFFIN and M. S.
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                                                                                         05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC079042; AAH79042.1; -G0; G0:0005869; C:dynactin complex; IEA. GO; G0:0007017; P:microtubule-based process; IEA.
                                                                                                                                                            Q6IRB3;
05-JUL-2004
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Mammalia; Eutheria; Rodentia;
                             Name=dctn2-prov;
                                                           Dctn2-prov protein.
                                                                                                                                                                                                                              Q6IRB3
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                                                                                                                                                                                                                              PRELIMINARY;
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(African clawed frog)
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1; Mismatches 0
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                                                                                                                                                                                                                           PRT;
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Rohas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R. W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
A Jones S. J. Marra M.A.
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070987; A.4H70987.1; -.
GO; GO:0005869; C.dynactin complex; IEA.
GO; GO:0007017; P:microtubule-based process; IEA.
InterPro; IPR006996; Dynamitin.
                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vej
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
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Name=MGC82128;
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                                      NCBI_TaxID=8355;
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403 AA; 44828
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Pred. No. 6e-14;
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ia; Pipoidea;
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RA Klausner R.D., Collins F.S., Wagner L., Shammen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Rabin G.M., Hong L.,

RA Bounstein M.J., Usdin T.B., Toshiyuki S., Cararinci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cararince P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay I.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Holkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Schmutz J., Myers R.M., Schein J.E.,

RA Alnes S. J. Marra M. A.
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Best Local
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Q7ZXY2;
01-JUN-2003
                                                                                                                                                                                                                                                                                                                          Detn2-prov protein.

Menopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).
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PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
Strausberg R.L., Feingold E.A., Shenmen C.M., S
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausmer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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                                                                                                                                                     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Pfam; PF04912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein S., Gerhard D.S.; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ EMBL; BC081081; AAH81081.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiative."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
                                                                                                                                                                                                               FROM
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4912; Dynamitin; 1.
403 AA; 44737 MW;
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82.7%;
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25,
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annotation update)
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A., Schein J.E.,
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RESULT 7
Q9PTG6
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Best Local &
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A., Gill S.R., Hasbani J., Crego C.;
Schroer T.A., Gill S.R., Hasbani J., Crego C.;
Schmitted (NOV-1999) to the EMBL/GenBank/DDBJ
EMBL, AF200744; AAF13996.1; -.
EMBL, AF200744; AAF13996.1; Complex; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9PTG6;
Q9PTG6;
01-MAY-2000
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Pfam; PF04912; Dynamitin; 1.
                                                                                                                                                                           "Role of dynactin in endocytic traffic: overexpression and colocalization with C Mol. Biol. Cell 10:4107-4120(1999)
                                                                                                                                                                                                                                                       MEDLINE=20056093; PubMed=10588646; Valetti C., Wetzel D.M., Schrader Kreis T.E., Schroer T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=p50;
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000
01-MAR-2003
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
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Neognathae; Galliformes; Phasianidae; Phasiani
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Pred. No. 4e-13;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3346E0F0F644B186 CRC64;
                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                process;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402
                                                                                                                                                                                                                                                                                   Hasbani M.J.,
                                                                                                                                                                                                        cLIP-170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Casavant T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE=2238527; PubMed=12477932; DOI=10.1073/pnas.242603899;

& Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

& Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

& Altschall S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

& Altschall S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

& Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

& Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

& Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

& Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

& Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

& Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Scheetz T.E.,

& Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

& Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

& Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

& Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

& Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

& Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

& Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

& Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

& Villalon D.K., Muzny D.M., Sodergren B.D., Dickson M.C.,

& Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

& Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

& Jones S. T. Mayra M.A.
                                                                                                                 Matches
                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ
EMBL; BC053120; AAH53120.1; -
ZFIN; ZDB-GENE-040426-1279; Zgc:63867.
GO; GO:0005869; C:dynactin complex; IEA.
GO; GO:0007011; P:microtubule-based process;
GO; GO:0007011; P:microtubule-based process;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7T3H1;
Q7T3H1;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Cyprinidae; Danio
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=zgc:63867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similar to dynactin 2 (P50).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
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                                                                                                                                                                                                                                                 Pro; IPR006996; Dynamitin.
PF04912; Dynamitin.
     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96
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                                                                                                                                            Similarity
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                                            GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKBSATEEKLTPVLLAKQLAAL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
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GVKETPOOKYORLVNEIHELCODVEKIQISTKESGABERLTPVALAQOAAQL 147
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                                                                                                                                                                                                                         44625 MW;
                                                                                                                                      70.5%;
67.3%;
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26,
                                                                                                        Score 177; DB
Pred. No. 1.2e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Pred. No. 1.2e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99:16899-16903 (2002)
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                                                                                                                                                                                                                            CA00047342500953 CRC64;
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                                                                                                                                         DB 2;
..2e-09;
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1.2e-09;
hes 9;
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                                                                                                           9;
                                                                                                                                                                    Length 405;
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                                                                                                           Indels
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RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Schapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abzamson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                 Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q6IP53;
Q6IP53;
05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                              Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DD
EMBL; BC072065; AAH72065.1; -.
GO; GO:0005874; C:microtubule; IEA.
GO; GO:0000226; P:microtubule cytoskeleton
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                 PRINTS; PR00511;
                                                                                                                                                                                                                                                                                          InterPro; IPR000435; Tektin. Pfam; PF03148; Tektin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=MGC78949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22341132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CISSUE=Embryo;
      336
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                                                                                                                                                Similarity
RLINEVQEITTNIERLRETLSQAETELK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                       RLLHEVQELTTEVEKIKTTVKESATEEK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225:384-391 (2002) .
                                                                                                                                                                                                                                     402
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(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic tools for Kenopus research: The NIH Kenopus
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                                                                                                                                                                                                                                                                 TEKTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12454917; DOI=10.1002/dvdy.10174; sberg R.L., Wagner L., Pontius J., Clifton S.W.,
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Pred. No. 16;
10; Mismatches
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RESULT 10 Q9V4Y9 ID Q9V4Y

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RA Adams C., Colinker S.E., Holt R.A., Evans C.A., Goayne J.D.,
RA Adams M.D., Celniker S.E., Hit R.A., Evans C.A., Goayne J.D.,
RA Manatides P.G., Scherer S.E., Hit R.A., Evans C.A., Goayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hallew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Hallew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Lauk C., Gaptella J., L., Lang J., Harris M.,
RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris M., Malasha F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA McIntol S., McIntosh T.C., McLeed M.P., McIberson D.,
RA McIntol S., McIntosh T.C., McLeed M.P., McHersii A.,
McPhal
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01-MAY-2000 (TrEMBLrel. 13
25-OCT-2004 (TrEMBLrel. 28
CGB269-PA (LD07994p).
Name=Dmn; ORFNames=CGB269;
                                                                                                                                                                                        Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Vente: Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchtromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                        SEQUENCE FAV...

SEQUENCE 23426070; Puonoc.

MEDLINE=23426070; Puonoc.

Meeler J.S., Bergman C.M., Kro....

Meeler D.A.,
                                    "The transposable elements of the Drosophila melanogaster euchromatin
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                    genomics
                  perspective."
3:RESEARCH0084-RESEARCH0084 (2002)
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0; PubMed=12537573;

Comman C.M., Kronmiller B., Car.

D.A., Lewis S.E., R
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Matches 19
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Q6MVP7;
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05-JUL-2004 (TrEMBLrel. 2
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05-JUL-2004 (TrEMBLrel. 2
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EMBL, AE001835, AAF59034 l; -.
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Stapleton M., bac
Stapleton M., Chavez C.,
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German Neurospora genome project;
Submitted (NOV-2003) to the EMBL/G
EMBL; BX842625; CAE76249.1; -.
GO; GO:0005525; F:GTP binding; IEA
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; P
Sordariomycetidae;
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יירא G., Mewes H.W., Manr
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Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Relkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
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Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
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Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
A Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
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Nature O:O-0(2003).
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InterPro; IPR004540; EF-G.C.
InterPro; IPR009022; EFG III V.

InterPro; IPR009022; EFG IVI V.

InterPro; IPR005517; EFG IV.

InterPro; IPR004161; EFFU D2.

InterPro; IPR00795; ProtSyn GTPb InterPro; IPR005255; Small GTP.
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Q7SH14;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
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Pfam; PF03764; EFG_TV; 1.

Pfam; PF030009; GTP_EFTU; 1.

Pfam; PF030004; GTP_EFTU D2; 1.

Pfam; PF03144; GTP_ETU D2; 1.

Pfam; PR03144; EFG_TV; 1.

PRINTS; PR00315; ELONGATNFCT.

TIGRPAMS; TIGR00231; small GTP; 1.

TIGRPAMS; TIGR00231; small GTP; 1.

Elongation factor; GTP-binding; Protein biosynthesis.

SEQUENCE 800 AA; 88373 MW; F2A7C425F6D4974A CRC64;
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01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
EMBL; AABX01000006; EAA36106.1;
HSSP; P13551; 1FNM.
GO; GO:0005525; F:GTP binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=NCU02955.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5141;
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                                                                   CAUTION: The sequence shown here EMBL/GenBank/DDBJ whole genome sh
                                                      preliminary data.
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:0005525; F:GTP binding; IEA
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hotgun (WGS)
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Neurospora.
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InterPro; IPR00640; EFG_III V.
InterPro; IPR009022; EFG_III V.
InterPro; IPR005517; EFG_IV.
InterPro; IPR005517; EFG_IV.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR009000; Translat_factor.
InterPro; IPR009000; Translat_factor.
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=JCM 10545 / 7;

MEDLINE=21456156; PubMed=11572479;

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Oshima T., Kikuchi H.;
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Q971V5;
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DNA Res. 8:123-140(2001).
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
Hypothetical protein ST1273.
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TIGRPAMS; TIGR00231; small GTP; 1.
PROSITE; PS00301; EFACTOR_GTP; 1.
GTP-binding; Hypothetical protein; Protein biosynthesis.
SEQUENCE 813 AA; 89810 MW; C9A5093F35B29B05 CRC64;
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Pfam; PF03764; EFG_IV; 1.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
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                                                                                                                                                                                                                                                                                 EMBL;
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GO:0006414;
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                                                VKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL
IKQLSQQK-QSLIQVISEIKKEFEQIKNVEK---VKEKLDPLQILKKIEQL 117
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                                                                                                                            27.9%;
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26.2%; Pred. No. 1e+0
tive 14; Mismatches
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11; Mismatches
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674338A5E031B429 CRC64;
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MEDLINE 2019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Helt G., Nelson C.R., Gabor G.L., A Barandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., A Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Bestova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Botkstein P., Brottier A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Calle C., Davies P., Davies P
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Matches 19
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Q86BS5;
01-JUN-2003
01-JUN-2003
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Q8MQK1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PROSITE; PS50945; I_LWEQ;
SEQUENCE 751 AA; 85362
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ORFNames=CG10971;
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GO; GO:0003779; F:actin binding;
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Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.A., Hostin D., Houston K.A., Helmann T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Helmann T.J., Wei M.H., Ibegwam C.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K.A., Saunders R.D., Scheeler F., Shen H., RA Syler E., Syradling A.C., Stapleton M., Strong R., Sun B., Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Zhong W., Zhong W., Zhong W., Zhou Q.A., Ye J., Weins R.A., Myers E.M., Rub, R., Shong W., Zhong G., Zhao Q., Zheng L., The genome sequence of Drosophila melanogaster.";

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                                                                                                                                                                                                                                                                                                                                                    MEDIJINE=22426069; PubMed=12537572;
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Hradecky P., Huang Y., Kaninker J.S., Millburn G.H., Prochnik S.E.
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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SEQUENCE FROM N.A.

MEDLINE=22426070; PubMed=12537573;

Kaminker J.S., Bergman C.M., Kronmiller B., Ca

Kaminker J.S., Wheeler D.A., Lewis S.E.,
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            FlyBase; FBgn036309; CG10971.
GO; GO:0003779; F:actin binding; IEA.
GO; GO:0005543; F:phospholipid binding;
InterPro; IPR011417; ANTH.
                                                                                              Submitted (MAR-2004) to the EMBL; AE003540; AAF49884.1;
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InterPro; IPR008943; PI_bind_N.
Pfam; PF07651; ANTH; 1.
Pfam; PF01608; I_LWEQ; 1.
ProDom; PD011820; ILWEQ; 1.
PROSITE; PS50942; ENTH; 1.
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length: 2000000000
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145.410 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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309
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                                                                                                 US-09-270-767-43370
US-09-902-540-114908
US-09-9137-9902-7806
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US-09-269-858A-8
US-09-269-858A-8
US-09-238-092-1321
US-09-248-796A-14974
US-09-943-948-14
US-09-073-541A-14
US-09-073-541A-14
US-09-073-541A-14
US-09-107-433-3720
US-09-107-433-3720
US-09-107-433-3720
US-08-478-337-6
US-08-478-373-6
US-08-478-373-6
US-08-478-373-6
US-08-487-518-6
US-08-639-518-6
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Sequence 14908,
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                      3, Ap
7454,
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US-09-270-767-43370
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58	58.5	58.5	58.5	58.5	59	59	59	59	59	59	59	59	59	59	59.5	59.5	59.5
23.1	23.3	23.3	23.3	23.3	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.7	23.7	23.7
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Sequence 8,		Sequence 64	Sequence 2,	Sequence 2,	Sequence 76	Sequence 76	Sequence 4,	Sequence 1,	Sequence 4,	Sequence 45	Sequence 18	Sequence 12	Sequence 13				
8, Appli	8325, Ap	6466, Ap	2, Appli	Appli	7647, Ap	7646, Ap		Appli	Appli	Appli	Appli	Appli	Appli	45139, A	æ	-	, Appl

ALIGNMENTS

Sequence 43370, Application US/09270767 Patent No. 6703491

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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Section and Application NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14908
                                       ; TYPE: PRT ; ORGANISM: Myxococcus xanthus US-09-902-540-14908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43370
LENGTH: 142
TYPE: PRT
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
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Best Local Similarity
                                                                                                           LENGTH:
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Query Match

Score 64.5;

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4.

Length 639;

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RESULT 4
US-09-107-532A-5587
; Sequence 5587, Application US/09107532A
; Patent NO. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm ar
: TITLE OF INVENTION: ENTEROCOCCUS FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Watches 17; Conserve
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US-09-513-999C-7806
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FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
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Matches 15; Conservative
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Patent No. 678396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
NAME/KEY: SIGNAL
LOCATION: -25..-1
OTHER INFORMATION: score
OTHER INFORMATION: seq i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
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SOFTWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: UNSURE LOCATION: 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 151
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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                                                                                                                                                                                                                                                                                                                                                                                                   86 KYKRLKAEVEKOSKKLEKKKETITESAGROOKKKIERQEEKL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                   9 KYQRLLHEVQELTTEVEKIKTTVKESA-----TESKL 40
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                                                                                                            CITY: Waltham
STATE: Massachusetts
                                                                                           COUNTRY: USA
                                                                                                                                                STREET: 100 Beaver Street
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ilarity 40.5%;
Conservative
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Pred. No.
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AND AMINO ACID SEQUENCES RELATING TO
FARCIUM FOR DIAGNOSTICS AND THERAPEUTICS
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NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...193
SEQUENCE DESCRIPTION: SEQ ID NO: 5587:
US-09-107-532A-5587
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                                                                               ; ORGANISM: Abedus herberti
US-09-269-858A-8
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Query Match 25.1%; Score 63; DB Best Local Similarity 30.9%; Pred. No. 28; Matches 17; Conservative 15; Mismatches
                                                                                                                                                               SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/269,858A CURRENT FILING DATE: 199-06-10 PRIOR APPLICATION NUMBER: PCT/EP97/05390 PRIOR FILING DATE: 1996-10-03 PRIOR APPLICATION NUMBER: EP/96115877 PRIOR FILING DATE: 1996-10-03 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Angerer, Bernhard
APPLICANT: Ankenbauer, Walt:
APPLICANT: Boehringer, M.
                                                                                                                   LENGTH: 85
TYPE: PRT
                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schmitz-Agheguian, Gudrun
APPLICANT: Svetlichny, Vitaly
TITLE OF INVENTION: Thermostable DNA Polymerase From Anaerocellum Thermophilum
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5587:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
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APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/ACENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELEPRON: (781)803-5007

TELEPRON: (781)803-507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                             Markau, Ursula
Reiser, Astrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ankenbauer, Waltraud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonch-Osmolovskaya, Elizaveta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 64; DB .
Pred. No. 3.9;
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                                     DB 4; Length 850;
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  19;
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  Indels
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  4.
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  Gaps
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192

GVKETPQQKYQRLLHE---VQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52

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RESULT 8
US-09-248-796A-14974
; Sequence 14974, Application US/09248796A
                                                                                                                                                             á
                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14203
US-09-538-092-1321
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US-09-623-326-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Anaerocellum thermophilum US-09-623-326-43
                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43, Application US/09623326 Patent No. 6607883
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1321
LENGTH: 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1321, Application US/09538092 Patent No. 6753314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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LENGTH: 851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Frey et al.
TITLE OF INVENTION: Polymerase Chimerase
FILE REFERENCE: 4894
CURRENT APPLICATION NUMBER: US/09/623,326
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: DE 198 10 879.6
PRIOR FILING DATE: 1998-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Giot, Loic APPLICANT: Mansfield,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using
FILE REFERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: CuraPatSeqFormatter Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                                             16;
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                                                                                                                                                               4 ETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GVKETPQQKYQRLLHE----VQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVKGIGEKSAQKLLEEYSSLEEIYQNLDKIKSSIREKLEAGK-DMAFLSKRLATI 245
                                                                                                                            ESLOQEVEALKERVDELTTDLEILKABIEEKGSDGAASSYQL-KQL 355
                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.1%; Score 63; DB 30.9%; Pred. No. 28; tive 15; Mismatches
                                                                                                                                                                                                                               24.9%; Score 62.5; 34.8%; Pred. No. 52;
                                                                                                                                                                                                           Mismatches
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SEQ ID NO 14974
LENGTH: 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wallis, Nicola G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Candida albicans
                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zalacain, Madgalenaa
APPLICANT: Throup, John
APPLICANT: Biswas, Sanjoy
TITLE OF INVENTION: Histidine Kinase
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 30-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch
CITY: Philadelphia
                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 41.2
les 14; Conservative
TOPOLOGY:
                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 EETPIQPDNPKRRILHEIIDLTSDTEDIEPTTPE 304
                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09081689
                                                          442 amino acids
                                                                                                                                         215-994-2222
  linear
                  single
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Pred. No. 13;
8; Mismatches
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APPLICANT: No. 6331407ak, Rodger
APPLICANT: Toumanen, Elaine
FITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF
FILE REFERENCE: 1340-1-016N1
CURRENT APPLICATION NUMBER: US/09/305,984B
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: 60/684,399
EARLIER APPLICATION NUMBER: 60/684,399
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 09/305,984
EARLIER FILING DATE: 1998-05-05
NUMBER: OF SEQ. ID NOS: 76
; Sequence 14,
                RESULT 12
US-09-493-940-14
                                                                                      문
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                                                                                                                                                                                                                              LENGTH: 442
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-073-541A-14
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                 SOFTWARE: 1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09073541A Patent No. 6448224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09305984B Patent No. 6331407
                                                                                                                                                          Matches
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: No. 6448224ak, Rodger
APPLICANT: Toumanen, Elaine
TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
FILE REFERENCE: 1340-1-016
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/073,541A
CURRENT FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 442
                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 LKÉQINSLYOHLLTVIADLHÉKNÉAILOLÉKMKVEFLRGÁSHÉLKTPLASLKIL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 LKEQINSLYQHLLTVIADLHEKNEAILQLEKMKVEFLRGASHELKTPLASLKIL 253
                                                                                      200 LKEQINSLYQHLLTVIADLHEKNEAILQLEKMKVEFLRGASHELKTPLASLKIL
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                                                                                                                     2 VKETPQQKYQRL-----LHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQL 49
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18; Conservative
                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.0
Application US/09493940
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                                                                                                                                                                        24.3%;
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                                                                                                                                                      ; Score 61; DB ; Pred. No. 23; 6; Mismatches
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; Pred. No. 23;
6; Mismatches
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Pred. No. 23;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
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                                                                                                                                                                                           Length 442;
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                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-107-433-3720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Streptococcus pneumoniae US-09-583-110-5317
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US-09-583-110-5317
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SEQ ID NO 5317
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 24.3%;
Best Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5317, A
Patent No. 66997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: No. 6630583ak, Rodger
APPLICANT: Toumanen, Elaine
TITLE OF INVENTION: NOVEL ANTIBIOTICS AND METHODS OF USING THE SAME
FILE REFERENCE: 1340-1-016N1
FULL REFERENCE: 1340-1-016N1
FUL
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NUMBER OF SEQ ID NOS: 76
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EARLIER APPLICATION NUMBER: 09/305,984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 442
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 LKEQINSLYQHLLTVIADLHEKNEAILQLEKMKVEFLRGASHELKTPLASLKIL 253
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ilarity 33.3%;
Conservative
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Pred. No. 23;
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; NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...446; SEQUENCE DESCRIPTION: SEQ ID NO: 3720: US-09-107-433-3720
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                                                                                                                                                                                                                                                                                                           equence 6, Application US/08487890A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5277
INFORMATION FOR SEQ ID NO: 3720:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
                                                                                                             CORRESPONDENCE
                                                                                                                              NUMBER OF SEQUENCES:
                                               STREET: CONTO
                                                                                                                                                               APPLICANT:
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                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                           204 LKEQINSLYOHLLTVIADLHEKNEAILQLEKMKVEFLRGASHELKTPLASLKIL 257
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CITY: Waltham
STATE: Massachusetts
                                                                                                                                                 INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: <Unknov
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OPERATING SYSTEM: <Unknown>
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                                                                                                                                                           Chong, Pele
Gray-Owen, Scott
Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
                                                                             6th Floor, 330 Unviersity Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                        Loosmore, Sheena
Harkness, Robin
                                                                                                                                                                                                                                          Schryvers, Anthony
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                                                                                              Sim & McBurney
                                                                                                                              Transferrin Receptor Genes
147
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                                                                    Query Match 24.3%;
Best Local Similarity 32.6%;
Matches 15; Conservative
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INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/148,968 FILING DATE: 08-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                    TELEPHONE: (416) 5
                                                                                                                                                                                  LENGTH: 644 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
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COMPUTER: IF
                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                    2 VKETPQQKYQRLLHEVQELTTEVB-----KIKTTVKESATEEKLT 41
                                                                                                                                                                                                                                                                                               (416) 595-1155
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                                                                                                                                                                                                                                                                                                                                   1038-466 MIS:jb
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                                                                                      Score 61; DB
Pred. No. 36;
                                                                        Mismatches
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                                                                                                           DB 1; Length 644;
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Search completed: November Job time: 27.6952 secs ω 2005, 22:05:56

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Gaps

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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251
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Copyright (c) 1993 - 2005 Compugen Ltd.
                    /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US11E_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US11E_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10E_PUB.pep:*
                                                                                                                                                                                                                                                                                                                  _6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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103	107	113	231	246	248	248	251	251	251	251	Score
41.0	42.6	45.0	92.0	98.0	98.8	98.8	100.0	100.0	100.0	100.0	Query Match
20	21	22	134	52	224	183	465	465	406	401	Query Match Length DB
10	10	-	<u>1</u>	10	16	10	14	9	10	16	•
US-09-782-816A-5	US-09-782-816A-4	US-09-782-816A-3	US-10-106-698-6730	US-09-782-816A-51	US-10-425-115-315831	US-09-782-816A-54	US-10-102-806-676	US-09-925-298-676	US-09-782-816A-53	US-10-408-765A-1369	ID
Sequence 5, Appli	Segmence 4. Appli	Semience 3 Appli	Sequence 6730. Ap	Sequence 51, Appl	Sequence 315831,	Sequence 54, Appl	Sequence 676, App	Sequence 676, App	Sequence 53, Appl	Sequence 1369, Ap	Description

45	. 44.	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	ì
64	64	64	64	64	64	64	64	64		65.5	65.5	66	66	67	67	67	67	68	68	70	70		70.5	71				76	81	88	93	98	,
5	5	5	5	25.5	•	•	•	•	•		•	•	•	•	26.7	٠	•	•	•	•		28.1	•	•	•	•	•	•	•	٠	•	•	
188	188	188	188	188	188	188	188	185	348	1837	576	386	13	2481	2478	2478	2478	2368	2368	1087	1087	356	348	14	380	380	53	15	16	17	18	19	. 1
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-10-176-918-	0-175-746-	-10-14	-10-123-	-10-121-	0-140-	0-028-072-	4-320-	US-10-842-740-3	-437-963-	9-493-	-424-	-10-282-122A-	09-78	10-2	US-10-470-048B-220	-69-	-09-81	-09-81	-09-81	97-143-2	-11-097-143	-10-425-114-	-10-425-115-2	-09-782-81	-11-097-143-4	-09-782-816A-	-09-782-816A-	2-81	2-816A-	2-816A-	US-09-782-816A-7	2-816A-	
e 2,	e 2,	equence 2,	equence 2,	e 2,	e 2,	ν,	e 12	æ	e 139			719	12, Api	e 43762	G	1296	5816,	1238	5635,	22869,	e 22866	e 63356,	e 2104	11,	40	56,	e 52,	e 10,	9	ω	æ	•	diameter .

ALIGNMENTS

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FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1369
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-1369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
                                                                                       Query Match 100.0%; Score 251; DB 16; Best Local Similarity 100.0%; Pred. No. 1.5e-19; Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1369, Application US/10408765A Publication No. US20040101874A1
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
  94
                         1 GVKGTPQQKYQRLLHEVQBLTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 145
                                                                                                                                       Length 401;
                                                                                            Indels
                                                                                            0
                                                                                            Gaps
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0

US-09-782-816A-53

RESULT 2

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APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-925-298-676
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                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 676, A
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR EILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR EILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 406
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                          NAME/KEY: SITE LOCATION: (5)
                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                   ocal Similarity
158 GVKETPOOKYORLLHEVOELTTEVEKIKTTVKESATEEKLTPVLLAKOLAAL 209
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                                                                                                                                                                                                                                                                                                                                                              465
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                     GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09925298 o. US20020039764A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09782816A
                                                                 100.0%; Score 251; DB 9; ilarity 100.0%; Pred. No. 1.8e-19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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Pred. No. 1.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                   Length 465;
                                                                 Indels
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RESULT 4 US-10-102-806-676

RESULT 6 US-10-425-115-315831

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CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 183
TYPE: PRT
ROANISM: Mus musculus
US-09-782-816A-54
                                                                                                                                                                                                                                                                                                                                          ; Sequence 54, Application US/09782816A
; Publication No. US20030032771A1
; GENERAL INFORMATION:
; APPLICANT: Sharp, David J.
; APPLICANT: Rogers, Gregory C.
; APPLICANT: Scholey, Jonathon M.
; APPLICANT: Scholey, Jonathon M.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF INVENTION: PROLIFERATION
; FILE REFERENCE: UC069.001A
                                                          Query Match
Best Local Similarity
Matches 51; Conserve
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US-09-782-816A-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 676, A Publication No.
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: SITE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE LOCATION: (16)
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LOCATION: (6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 465
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0%; es 52; Conservarion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 209
    94
                           1 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL
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GVKETPOOKYORLLHEVOELTTEVEKIKTTVKESATEEKLTPVVLAKOLAAL 145
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o. US20030054421A1
                                                                               Conservative
                                                                                                98.8%;
98.1%;
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                                                                             Score 248; DB 10;
Pred. No. 1.3e-19;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 251; DB 14;
Pred. No. 1.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                               Indels
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RESULT 8
US-10-106-698-6730
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US-10-425-115-315831
             GENERAL INFORMATION:
APPLICANT: Ruben et
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERBYCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 315831
TENETH 224
                                                                      Sequence 6730, Application US/10106698
Publication No. US20030109690A1
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51, Application US/09782816A Publication No. US20030032771A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UCC69.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yihua
                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: UNSURE
LOCATION: 44
COTHER INFORMATION: Xaa = Val or Leu
OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
OTHER INFORMATION: musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 52
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                                                                                                                                                                                                                            1 GVKETPQQKYQRLLHEVQELTTEVEKIKTTVKESATEEKLTPVLLAKQLAAL 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 98.8%; Similarity 98.1%; 51; Conservative
                                                                                                                                                                                                                                                                                 h 98.0%;
Similarity 98.1%;
51; Conservative
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al.
Colon and Colon Cancer Associated Polynucleotides and Polypeptide
                                                                                                                                                                                                                                                                                 Score 246; DB 1
Pred. No. 5e-20;
0; Mismatches
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Pred. No. 1.7e-19;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                           Length 52;
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RESULT 10 US-09-782-816A-4

Sequence 4, Application US/09782816A
publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION

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US-09-782-816A-3
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CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REPERENCE: UC069,001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 22
TURNEL TO THE TOTAL T
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APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09782816A Publication No. US20030032771A1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: A sequence conserved OTHER INFORMATION: musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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NAME/KEY: MISC FEATURE
LOCATION: (126)
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                                                                                                                                                         Local Similarity
nes 22; Conserv
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                                             1 GVKETPQQKYQRLLHEVQELTT 22
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GVKETPQQKYQRLLHEVQELTT 22
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                                                                                                                                                                                          Score 113; DB 10; Pred. No. 1.1e-05;
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Pred. No. 7.1e-18;
                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF CELLULAR
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                                                                                                                                                                                                                               Length 22
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APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Rogers, Gregory C.
APPLICANT: Rogers, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE RETERENCE: UC050,001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 20
TYPE: PRT
ORGANIEM: Unknown
                                                  Sequence 1, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CEI
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
CURRENT APPLICATION UMMBER: US/09/782,816A
CURRENT APPLICATION UMMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEO ID NOS: 56
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US-09-782-816A-1
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; OTHER INFORMATION: A sequence
; OTHER INFORMATION: musculus.
US-09-782-816A-5
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; OTHER INFORMATION:
US-09-782-816A-4
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; LENGTH: 21
; TYPE: PRT
ORGANISM: Unknown
; FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09782816A Publication No. US20030032771A1 GENERAL INFORMATION:
              SOFTWARE: FastSEQ for SEQ ID NO 1
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Best Local Similarity
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
LENGTH: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           41.0%; 2-
100.0%; Pred. No.
ive 0; Mismatches
                                     Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.6%; Score 107; DB 10; 100.0%; Pred. No. 4.7e-05; Live 0; Mismatches 0;
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                                                                                                                                                           CELLULAR
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US-09-782-816A-6
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SEQ ID NO 6
LENGTH: 19
                                                                    FILE REFERENCE: UC069.001A
CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                          Sequence 7, Application US/09782816A Publication No. US20030032771A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                              APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEDTIDE INHIBITORS
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sharp, David J.
APPLICANT: Rogers, Gregory C.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC069.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/782,816A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: A sequence conserved OTHER INFORMATION: musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Unknown
FEATURE:
               TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa = Val or Leu
OTHER INFORMATION: The sequence is a Homo sapiens sequence when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: UNSURE
FEATURE:
                                                    ENGTH: 18
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les 22; Conserv
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95.7%;
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100.0%; Pred. No.
cive 0; Mismatc
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Pred. No. 0.00015;
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. 0.00042;
ches 0;
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Sequence 8, Application US/09782816A
Publication No. US20030032771A1
GENERAL INFORMATION:
APPLICANT: Sharp, David J.
APPLICANT: Scholey, Jonathon M.
APPLICANT: Scholey, Jonathon M.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CELLULAR
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: UC669.001A
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
SEQ ID NO 8
SEQ ID NO 8
FEATURE:
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: A sequence conserved among Homo sapiens and Mus
OTHER INFORMATION: musculus.
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Search completed: November 3, 2005, 22:11:40 Job time: 94.7112 secs
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US-09-782-816A-8
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                                                                                                                                 Query Match

35.1%; Score 88; DB 10; Length 17; The length 17; The length 17; The length 17; Conservative 0; Mismatches 0; Indels 0; Gans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.1%; Score 93; DB 10; Length 18; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                            0
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